

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.2326 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 0

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	NaN	1	2	ADD95004 Platelet
2	0	NaN	1	2	ADD94992 Platelet
3	0	NaN	1	2	ADD94993 Platelet
4	0	NaN	1	2	ADD95002 Platelet
5	0	NaN	1	2	ADD94997 Platelet
6	0	NaN	1	2	ADD94999 Platelet
7	0	NaN	1	2	ADD95003 Platelet
8	0	NaN	1	2	ADD94995 Platelet
9	0	NaN	1	2	ADD94998 Platelet
10	0	NaN	1	2	ADD95001 Platelet
11	0	NaN	1	2	ADD94990 Platelet
12	0	NaN	1	2	ADD94991 Platelet
13	0	NaN	1	2	ADD94994 Platelet
14	0	NaN	1	2	ADD94996 Platelet
15	0	NaN	1	2	ADD95000 Platelet
16	0	NaN	1	2	AAY46852 Immunogen
17	0	NaN	1	4	AAM97834 Human pep
18	0	NaN	1	4	AAM97974 Human pep
19	0	NaN	1	4	AAM97643 Human pep
20	0	NaN	1	4	AAM98447 Human pep
21	0	NaN	1	4	AAM98354 Human pep
22	0	NaN	1	4	AAM53290 Human non
23	0	NaN	1	4	AAM53329 Human non
24	0	NaN	1	4	AAM53291 Human non

25	0	NaN	1	4	AAM53328	Human non
26	0	NaN	1	4	AAM53219	Human non
27	0	NaN	1	4	AAM53218	Human non
28	0	NaN	1	4	AAB91029	Thyrotrop
29	0	NaN	1	4	AAB91739	Oploid pe
30	0	NaN	1	4	AAB92150	Polypepti
31	0	NaN	1	4	AAB91892	Apoptosis
32	0	NaN	1	4	AAB91546	Endotheli
33	0	NaN	1	4	AAB92392	Miscellan
34	0	NaN	1	4	AAB91665	Oploid pe
35	0	NaN	1	4	AAG99966	ERA bindi
36	0	NaN	1	4	AAM00011	ERA bindi
37	0	NaN	1	4	AAG99987	ERA bindi
38	0	NaN	1	4	AAG99983	ERA bindi
39	0	NaN	1	4	AAM00013	ERA bindi
40	0	NaN	1	4	AAM00016	ERA bindi
41	0	NaN	1	4	AAG99988	ERA bindi
42	0	NaN	1	4	AAM00010	ERA bindi
43	0	NaN	1	4	ABB66809	Drosophil
44	0	NaN	1	4	ABB66810	Drosophil
45	0	NaN	1	4	AAG98134	Human SNP

ALIGNMENTS

RESULT 1
ADD95004
ID ADD95004 standard; peptide; 1 AA.
AC ADD95004;
XX
XX 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #146.
XX
KW Platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)."
FT
FT
XX
XX WO9501371-A1.
XX
XX 12-JAN-1995.
XX
XX 22-JUN-1994; 94WO-JP000999.
XX
XX 30-JUN-1993; 93JP-00186755.
XX
XX (YAWA) NIPPON STEEL CORP.
XX
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX
XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
XX
XX Disclosure; Page 11; 34pp; Japanese.
XX
XX The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.

SQ Sequence 1 AA;

Query Match NaN%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 2

ADD94992
 ID ADD94992 standard; peptide; 1 AA.

XX AC ADD94992;

XX DT 29-JAN-2004 (first entry)

XX DE Platelet aggregation inhibitor peptide #134.

XX KW platelet aggregation inhibitor; guanidino group; amidino group.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT /label= OTHER

XX FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"

XX FN WO9501371-A1.

XX PD 12-JAN-1995.

XX PF 22-JUN-1994; 94WO-JP000999.

XX PR 30-JUN-1993; 93JP-00186755.

XX -PA (YAWA) NIPPON STEEL CORP.

XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;

XX DR WPI; 1995-060950/08.

XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
 guanidino or amidino gp. at N-terminal to increase stability.

XX FS Disclosure; Page 10; 34pp; Japanese.

XX CC The invention describes peptides of amino acid sequence (I) and their
 salts. (I) are useful as platelet aggregation inhibitors and are easily
 absorbed by the body. Due to the presence of the N-terminal guanidino or
 amidino group, (I) are provided with excellent stability so that their
 activity can be exhibited for an effective time after administration.
 CC CC Thereafter they are readily metabolised and expelled. This is the amino
 acid sequence of a platelet aggregation inhibitor peptide.

SQ Sequence 1 AA;

Query Match NaN%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 3

ADD94993
 ID ADD94993 standard; peptide; 1 AA.

XX

AC ADD94993;

XX DT 29-JAN-2004 (first entry)

XX DE Platelet aggregation inhibitor peptide #135.

XX KW platelet aggregation inhibitor; guanidino group; amidino group.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT /label= OTHER

XX FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"

XX FN WO9501371-A1.

XX PD 12-JAN-1995.

XX PF 22-JUN-1994; 94WO-JP000999.

XX PR 30-JUN-1993; 93JP-00186755.

XX -PA (YAWA) NIPPON STEEL CORP.

XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;

XX DR WPI; 1995-060950/08.

XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
 guanidino or amidino gp. at N-terminal to increase stability.

XX PS Disclosure; Page 10; 34pp; Japanese.

XX CC The invention describes peptides of amino acid sequence (I) and their
 salts. (I) are useful as platelet aggregation inhibitors and are easily
 absorbed by the body. Due to the presence of the N-terminal guanidino or
 amidino group, (I) are provided with excellent stability so that their
 activity can be exhibited for an effective time after administration.
 CC CC Thereafter they are readily metabolised and expelled. This is the amino
 acid sequence of a platelet aggregation inhibitor peptide.

SQ Sequence 1 AA;

Query Match NaN%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 4

ADD95002
 ID ADD95002 standard; peptide; 1 AA.

XX AC ADD95002;

XX DT 29-JAN-2004 (first entry)

XX DE Platelet aggregation inhibitor peptide #144.

XX KW platelet aggregation inhibitor; guanidino group; amidino group.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT /label= OTHER

XX FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"

XX PN WO9501371-A1.
 XX PD 12-JAN-1995.
 XX PF 22-JUN-1994; 94WO-JP0000999.
 XX PR 30-JUN-1993; 93JP-00186755.
 XX PA (YAWA) NIPPON STEEL CORP.
 XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
 XX WPI; 1995-060950/08.
 DR
 XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain
 PT guanidino or amidino gp. at N-terminal to increase stability.
 XX PS Disclosure; Page 10-11; 34pp; Japanese.
 XX CC The invention describes peptides of amino acid sequence (I) and their
 CC salts. (I) are useful as platelet aggregation inhibitors and are easily
 CC absorbed by the body. Due to the presence of the N-terminal guanidino or
 CC amidino group, (I) are provided with excellent stability so that their
 CC activity can be exhibited for an effective time after administration.
 CC Thereafter they are readily metabolised and expelled. This is the amino
 CC acid sequence of a platelet aggregation inhibitor peptide.
 XX SQ Sequence 1 AA;
 Query Match NAN%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 R 1
 RESULT 5
 ADD94997
 ID ADD94997 standard; peptide; 1 AA.
 XX AC ADD94997;
 XX DT 29-JAN-2004 (first entry)
 XX DE Platelet aggregation inhibitor peptide #139.
 XX KW platelet aggregation inhibitor; guanidino group; amidino group.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
 FT defined)"
 XX PN WO9501371-A1.
 XX PD 12-JAN-1995.
 XX PF 22-JUN-1994; 94WO-JP0000999.
 XX PR 30-JUN-1993; 93JP-00186755.
 XX PA (YAWA) NIPPON STEEL CORP.
 XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
 XX WPI; 1995-060950/08.
 DR
 XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain
 PT guanidino or amidino gp. at N-terminal to increase stability.
 XX PS Disclosure; Page 10-11; 34pp; Japanese.
 XX CC The invention describes peptides of amino acid sequence (I) and their
 CC salts. (I) are useful as platelet aggregation inhibitors and are easily
 CC absorbed by the body. Due to the presence of the N-terminal guanidino or
 CC amidino group, (I) are provided with excellent stability so that their
 CC activity can be exhibited for an effective time after administration.
 CC Thereafter they are readily metabolised and expelled. This is the amino
 CC acid sequence of a platelet aggregation inhibitor peptide.
 XX SQ Sequence 1 AA;
 Query Match NAN%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 R 1
 RESULT 5
 ADD94997
 ID ADD94997 standard; peptide; 1 AA.
 XX AC ADD94997;
 XX DT 29-JAN-2004 (first entry)
 XX DE Platelet aggregation inhibitor peptide #139.
 XX KW platelet aggregation inhibitor; guanidino group; amidino group.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
 FT defined)"
 XX PN WO9501371-A1.
 XX PD 12-JAN-1995.
 XX PF 22-JUN-1994; 94WO-JP0000999.
 XX PR 30-JUN-1993; 93JP-00186755.
 XX PA (YAWA) NIPPON STEEL CORP.
 XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
 XX WPI; 1995-060950/08.
 DR
 XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain
 PT guanidino or amidino gp. at N-terminal to increase stability.
 XX PS Disclosure; Page 10; 34pp; Japanese.
 XX CC The invention describes peptides of amino acid sequence (I) and their
 CC salts. (I) are useful as platelet aggregation inhibitors and are easily
 CC absorbed by the body. Due to the presence of the N-terminal guanidino or
 CC amidino group, (I) are provided with excellent stability so that their
 CC activity can be exhibited for an effective time after administration.
 CC Thereafter they are readily metabolised and expelled. This is the amino
 CC acid sequence of a platelet aggregation inhibitor peptide.
 XX SQ Sequence 1 AA;
 Query Match NAN%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 R 1
 RESULT 6
 ADD94999
 ID ADD94999 standard; peptide; 1 AA.
 XX AC ADD94999;
 XX DT 29-JAN-2004 (first entry)
 XX DE Platelet aggregation inhibitor peptide #141.
 XX KW platelet aggregation inhibitor; guanidino group; amidino group.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
 FT defined)"
 XX PN WO9501371-A1.
 XX PD 12-JAN-1995.
 XX PF 22-JUN-1994; 94WO-JP0000999.
 XX PR 30-JUN-1993; 93JP-00186755.
 XX PA (YAWA) NIPPON STEEL CORP.
 XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
 XX WPI; 1995-060950/08.
 DR
 XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain
 PT guanidino or amidino gp. at N-terminal to increase stability.
 XX PS Disclosure; Page 10; 34pp; Japanese.
 XX CC The invention describes peptides of amino acid sequence (I) and their
 CC salts. (I) are useful as platelet aggregation inhibitors and are easily
 CC absorbed by the body. Due to the presence of the N-terminal guanidino or
 CC amidino group, (I) are provided with excellent stability so that their
 CC activity can be exhibited for an effective time after administration.
 CC Thereafter they are readily metabolised and expelled. This is the amino
 CC acid sequence of a platelet aggregation inhibitor peptide.
 XX SQ Sequence 1 AA;

PT New RGD peptide(s) useful as anti-platelet aggregation agents - contain
 PT guanidino or amidino gp. at N-terminal to increase stability.
 XX PS Disclosure; Page 10; 34pp; Japanese.
 XX CC The invention describes peptides of amino acid sequence (I) and their
 CC salts. (I) are useful as platelet aggregation inhibitors and are easily
 CC absorbed by the body. Due to the presence of the N-terminal guanidino or
 CC amidino group, (I) are provided with excellent stability so that their
 CC activity can be exhibited for an effective time after administration.
 CC Thereafter they are readily metabolised and expelled. This is the amino
 CC acid sequence of a platelet aggregation inhibitor peptide.
 XX SQ Sequence 1 AA;
 Query Match NAN%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 R 1
 RESULT 6
 ADD94999
 ID ADD94999 standard; peptide; 1 AA.
 XX AC ADD94999;
 XX DT 29-JAN-2004 (first entry)
 XX DE Platelet aggregation inhibitor peptide #141.
 XX KW platelet aggregation inhibitor; guanidino group; amidino group.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
 FT defined)"
 XX PN WO9501371-A1.
 XX PD 12-JAN-1995.
 XX PF 22-JUN-1994; 94WO-JP0000999.
 XX PR 30-JUN-1993; 93JP-00186755.
 XX PA (YAWA) NIPPON STEEL CORP.
 XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
 XX WPI; 1995-060950/08.
 DR
 XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain
 PT guanidino or amidino gp. at N-terminal to increase stability.
 XX PS Disclosure; Page 10; 34pp; Japanese.
 XX CC The invention describes peptides of amino acid sequence (I) and their
 CC salts. (I) are useful as platelet aggregation inhibitors and are easily
 CC absorbed by the body. Due to the presence of the N-terminal guanidino or
 CC amidino group, (I) are provided with excellent stability so that their
 CC activity can be exhibited for an effective time after administration.
 CC Thereafter they are readily metabolised and expelled. This is the amino
 CC acid sequence of a platelet aggregation inhibitor peptide.
 XX SQ Sequence 1 AA;

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Query Match      NaN%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 X 1
Db      1 R 1

RESULT 7
ADD95003
ID      ADD95003 standard; peptide; 1 AA.
XX
AC      ADD95003;
XX
DT      29-JAN-2004 (first entry)
XX
DE      Platelet aggregation inhibitor peptide #145.
XX
KW      platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS      Unidentified.
XX
FH      Key      Location/Qualifiers
FT      Modified-site 1
FT      /label= OTHER
FT      /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT      defined)"
XX
PN      WO9501371-A1.
XX
PD      12-JAN-1995.
XX
PF      22-JUN-1994; 94WO-JP000999.
XX
PR      30-JUN-1993; 93JP-00186755.
XX
PA      (YAWA ) NIPPON STEEL CORP.
XX
PI      Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
XX      WPI; 1995-060950/08.
XX
XX      New RGD peptide(s) useful as anti:platelet aggregation agents - contain
XX      guanidino or amidino gp. at N-terminal to increase stability.
XX
XX      Disclosure; Page 11; 34pp; Japanese.
XX
XX      The invention describes peptides of amino acid sequence (I) and their
XX      salts. (I) are useful as platelet aggregation inhibitors and are easily
XX      absorbed by the body. Due to the presence of the N-terminal guanidino or
XX      amidino group, (I) are provided with excellent stability so that their
XX      activity can be exhibited for an effective time after administration.
XX      Thereafter they are readily metabolised and expelled. This is the amino
XX      acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ      Sequence 1 AA;

Query Match      NaN%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 X 1
Db      1 R 1

RESULT 9
ADD94998
ID      ADD94998 standard; peptide; 1 AA.
XX
AC      ADD94998;
XX
DT      29-JAN-2004 (first entry)
XX
DE      Platelet aggregation inhibitor peptide #140.
XX
KW      platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS      Unidentified.
XX
FH      Key      Location/Qualifiers
FT      Modified-site 1
FT      /label= OTHER
FT      /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT      defined)"
XX
PN      WO9501371-A1.
XX

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XX	Disclosure; Page 10; 34pp; Japanese.
PS	
CC	"The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration.
CC	Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide."
CC	
XX	Sequence 1 AA;
SQ	
	Query Match NaN%; Score 0; DB 2; Length 1; Best Local Similarity 0.0%; Pred. NO. 0; Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps
QY	1 X 1
D6	1 R 1
RESULT 11	
ADD94990	standard; peptide; 1 AA.
ID	ADD94990 standard; peptide; 1 AA.
XX	
AC	ADD94990;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	platelet aggregation inhibitor peptide #132.
XX	
KW	platelet aggregation inhibitor; guanidino group; amidino group.
XX	
OS	Unidentified.
FH	Key Location/Qualifiers
FT	Modified-site 1
FT	/label= OTHER
FT	/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"
FT	
PN	WO9501371-A1.
XX	
PD	12-JAN-1995.
XX	
PF	22-JUN-1994; 94WO-JP000999.
XX	
PR	30-JUN-1993; 93JP-00186755.
XX	
PA	(YAWA) NIPPON STEEL CORP.
XX	
PI	Sato Y, Hayashi.Y, Katada J, Takiguchi Y;
XX	WPI; 1995-060950/08.
DR	
XX	New RGD peptide(s) useful as anti-platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
PT	
XX	
PS	Disclosure; Page 10; 34pp; Japanese.
XX	
CC	The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration.
CC	Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide."
CC	
XX	Sequence 1 AA;
SQ	
	Query Match NaN%; Score 0; DB 2; Length 1; Best Local Similarity 0.0%; Pred. No. 0;

DE	platelet aggregation inhibitor peptide #136.
XX	
KW	platelet aggregation inhibitor; guanidino group; amidino group.
XX	
OS	Unidentified.
XX	
PH	Location/Qualifiers
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FT	/label= OTHER
FT	/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"
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FT	
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PD	12-JAN-1995.
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XX	22-JUN-1994; 94WO-JP000999.
PF	
XX	
PR	30-JUN-1993; 93JP-00186755.
XX	
XX	(YAMA) NIPPON STEEL CORP.
PA	
XX	
PI	Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX	
DR	WPI; 1995-060950/08.
XX	
PT	New RGD peptide(s) useful as anti:platelet aggregation agents -
PT	guanidino or amidino gp. at N-terminal to increase stability.
PT	
XX	
PS	Disclosure; Page 10; 34pp; Japanese.
CC	
CC	The invention describes peptides of amino acid sequence (I) and
CC	salts. (I) are useful as platelet aggregation inhibitors and are
CC	absorbed by the body. Due to the presence of the N-terminal guan
CC	amidino group, (I) are provided with excellent stability so that
CC	activity can be exhibited for an effective time after administra
CC	thereafter they are readily metabolised and expelled. This is th
CC	acid sequence of a platelet aggregation inhibitor peptide.
XX	
SQ	Sequence 1 AA;
	Query Match NaN%; Score 0; DB 2; Length 1;
	Best Local Similarity 0.0%; Pred No. 0;
	Matches 0; Conservative 0; Mismatches 1; Indels 0;
OY	1 X 1
DB	1 R 1
RESULT 14	
ADD94996	
ID	ADD94996 standard; peptide; 1 AA.
XX	
AC	ADD94996;
XX	
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Platelet aggregation inhibitor peptide #138.
XX	
KW	platelet aggregation inhibitor; guanidino group; amidino group.
XX	
OS	Unidentified.
XX	
PH	Location/Qualifiers
FT	1
FT	/label= OTHER
FT	/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"
FT	
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XX	WO9501371-Al.
PN	
XX	
PD	12-JAN-1995.

XX PF 22-JUN-1994; 94WO-JP000999.
XX PR 30-JUN-1993; 93JP-00186755.
XX PA (YAWA) NIPPON STEEL CORP.
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX PI WPI; 1995-060950/08.
XX DR
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
XX PT guanidino or amidino gp. at N-terminal to increase stability.
XX PS Disclosure; Page 10; 34pp; Japanese.
XX CC The invention describes peptides of amino acid sequence (I) and their
XX CC salts. (I) are useful as platelet aggregation inhibitors and are easily
XX CC absorbed by the body. Due to the presence of the N-terminal guanidino or
XX CC amidino group, (I) are provided with excellent stability so that their
XX CC activity can be exhibited for an effective time after administration.
XX CC Thereafter they are readily metabolised and expelled. This is the amino
XX CC acid sequence of a platelet aggregation inhibitor peptide.
XX SQ Sequence 1 AA;
Query Match NaN; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 R 1
RESULT 15
ADD95000
ID ADD95000 standard; peptide; 1 AA.
XX AC ADD95000;
XX DT 29-JAN-2004 (first entry)
XX DE Platelet aggregation inhibitor peptide #142.
XX KW platelet aggregation inhibitor; guanidino group; amidino group.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /label= OTHER
XX FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
XX FT defined)"
XX PN WO9501371-A1.
XX PD 12-JAN-1995.
XX PF 22-JUN-1994; 94WO-JP000999.
XX PR 30-JUN-1993; 93JP-00186755.
XX PA (YAWA) NIPPON STEEL CORP.
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX PI WPI; 1995-060950/08.
XX DR
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
XX PT guanidino or amidino gp. at N-terminal to increase stability.
XX PS Disclosure; Page 10; 34pp; Japanese.

XX CC The invention describes peptides of amino acid sequence (I) and their
XX CC salts. (I) are useful as platelet aggregation inhibitors and are easily
XX CC absorbed by the body. Due to the presence of the N-terminal guanidino or
XX CC amidino group, (I) are provided with excellent stability so that their
XX CC activity can be exhibited for an effective time after administration.
XX CC Thereafter they are readily metabolised and expelled. This is the amino
XX CC acid sequence of a platelet aggregation inhibitor peptide.
XX SQ Sequence 1 AA;
Query Match NaN; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 R 1
Search completed: May 2, 2006, 08:54:56
Job time : 91.2326 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 14.5116 Seconds

(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 0

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	0	Nan	3	3	A22565		R-phycoerythrin al
2	0	Nan	3	3	PQ0010		angiotensin-conver
3	0	Nan	3	3	S13894		histidinol dehydro
4	0	Nan	3	3	A43391		TRH-like tripeptid
5	0	Nan	3	3	E37196		bradykinin-potent
6	0	Nan	3	3	F37196		bradykinin-potent
7	0	Nan	3	3	I50412		gene p20K protein
8	0	Nan	3	3	PT0636		T-cell receptor be
9	0	Nan	3	3	PT0578		T-cell receptor be
10	0	Nan	3	3	PT0571		T-cell receptor be
11	0	Nan	3	3	PT0622		T-cell receptor be
12	0	Nan	3	3	I78890		tyrosine protein k
13	0	Nan	3	3	S68328		blood cell protein
14	0	Nan	3	3	T13892		cytochrome-c oxida
15	0	Nan	3	3	GRGU		growth-modulating
16	0	Nan	3	3	RHPGT		thryoliberin - pig
17	0	Nan	3	3	A60898		burstin - chicken
18	0	Nan	3	3	A23751		spinal cord peptid
19	0	Nan	3	3	B23751		spinal cord peptid
20	0	Nan	3	3	A33802		thyrortropin-releas
21	0	Nan	3	3	RHSHT		thryoliberin - she
22	0	Nan	3	3	A92971		thryoliberin - eas
23	0	Nan	3	3	RHTDFO		thryoliberin - Bom
24	0	Nan	4	1	ECXAA		antho-RFamide neur
25	0	Nan	4	2	S18401		thyroglobulin - do
26	0	Nan	4	2	A02147		phagocytosis-stimu
27	0	Nan	4	2	A37832		phenol 2-monooxyge
28	0	Nan	4	2	A48360		gamma subunit of P
29	0	Nan	4	2	A61300		22K superhelical P

30 0 Nan 4 2 A41890 protein D - Escher
31 0 Nan 4 2 S43014 hypotheical prote
32 0 Nan 4 2 D41654 hypotheical prote
33 0 Nan 4 2 B43848 cell surface adhe
34 0 Nan 4 2 I40505 hypotheical prote
35 0 Nan 4 2 I40370 phospholipase C (E
36 0 Nan 4 2 T46827 hypotheical prote
37 0 Nan 4 2 S53508 starvation-induced
38 0 Nan 4 2 A27897 glucan 1,4-alpha-g
39 0 Nan 4 2 T30569 hypotheical prote
40 0 Nan 4 2 I38888 COI intron 16 prot
41 0 Nan 4 2 A25844 RPCH-related neuro
42 0 Nan 4 2 A34826 metallothionein-A
43 0 Nan 4 2 I51049 myosin-light-chain
44 0 Nan 4 2 S39390 protamine Pl - ora
45 0 Nan 4 2 I61883

ALIGNMENTS

RESULT 1

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>
A:Cross-references: UNIPARC:UPI000017CE9A

Query Match Nan%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 2 Y 2

RESULT 2

PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N:Alternate names: ficus latex peptide 3
C:Species: Ficus carica (common fig)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PQ0010
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0008
A:Accession: PQ0010
A:Molecule type: protein
A:Residues: 1-3 <MAR>
A:Cross-references: UNIPARC:UPI000011E971
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match Nan%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 L 1

RESULT 3

S13894
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: S13894
R:Nagai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A:Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A:Reference number: S13894; MUID:91112783; PMID:1989490
A:Accession: S13894
A:Molecule type: protein
A:Residues: 1-3 <NAG>
A:Cross-references: UNIPARC:UPI000017CE9B
A:Experimental source: var. capitata
C:Keywords: dimer; NAD; oxidoreductase

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 X 1

RESULT 4
A43391
TRH-like tripeptide - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A43391
R:Lackey, D.B.
J. Biol. Chem. 267, 17508-17511, 1992
A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-
A:Reference number: A43391; MUID:92388092; PMID:1517203
A:Accession: A43391
A:Molecule type: protein
A:Residues: 1-3 <LAC>
A:Cross-references: UNIPARC:UPI000017CE9C
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 5
E37196
bradykinin-potentiating peptide 5 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C:Accession: E37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides f
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: E37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
A:Cross-references: UNIPARC:UPI0000158403
A:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 6
F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: F37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: F37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
A:Cross-references: UNIPARC:UPI000017CE9D
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 7
I50412
gene p20K protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I50412
R:Mao, P.L.; Beauchemin, M.; Bedard, P.A.
J. Biol. Chem. 268, 8131-8139, 1993
A:Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicke
A:Reference number: A46643; MUID:93216790; PMID:8463325
A:Accession: I50412
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-3 <MAO>
A:Cross-references: UNIPARC:UPI00000618AB; GB:L02537; NID:G212616; PID:G212617
C:Genetics:
A:Gene: p20K

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 2 S 2

RESULT 8
PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PT0636
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0636
A:Status: translation not shown
A:Molecule type: mRNA

```
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CE9E
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match      NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 A 1

RESULT 9
PT0578
T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0578
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0578
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CE9F
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match      NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 A 1

RESULT 10
PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0571
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0571
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CEA0
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match      NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 A 1

RESULT 11
PT0622
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: PT0622; PT0680; PT0582; PT0673
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0622
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CEA1
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P
A;Accession: PT0680
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-3 <FEE1>
A;Cross-references: UNIPARC:UPI000017CEA1
A;Experimental source: day 18 fetal thymus, strain BALB/c clones 154-1J and 154-1F
A;Accession: PT0582
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE2>
A;Cross-references: UNIPARC:UPI000017CEA1
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A
C;Keywords: T-cell receptor

Query Match      NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 A 1

RESULT 12
I78890
Tyrosine protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: I78890
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, (
Oncogene 9, 3437-3448, 1994
A;Title: Two distinct protein isoforms are encoded by ntck, a csk-related tyrosine prot
A;Reference number: I58407; MUID:95060800; PMID:7970703
A;Accession: I78890
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3 <RES>
A;Cross-references: UNIPARC:UPI000011E834; GB:I33339; NID:G609536; PIDN:AAA64432.1; PII
C;Genetics:
A;Gene: p52ntk

Query Match      NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      3 T 3

RESULT 13
S68328
blood cell protein A -- Molgula manhattensis (fragment)
C;Species: Molgula manhattensis
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S68328
R;Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995
A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from
A;Reference number: S68325; MUID:96132650; PMID:8554314
A;Accession: S68328
A;Molecule type: Protein
```

A:Residues: 1-3 <TAY>

A:Cross-references: UNIPARC:UPI000017CBA2

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 A 1

RESULT 14

T13892
cytochrome-c oxidase (BC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (frag
C:Species: mitochondrion lampetra fluviatilis (river lamprey)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: T13892
R:DeLaunay, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
A:Reference number: Z17775; MUID:97398704; PMID:9254918
A:Accession: T13892
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-3
A:Cross-references: UNIPARC:UPI000011E981; EMBL:Y09528; NID:G2340016; PID:CAA70721.1; F
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 2 T 2

RESULT 15

GKHU
growth-modulating peptide - human
C:Species: Homo sapiens (man)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C:Accession: A01421
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A:Reference number: A01421; MUID:77162369; PMID:858356
A:Accession: A01421
A:Molecule type: protein
A:Residues: 1-3 <SCH>
A:Cross-references: UNIPARC:UPI000012BB5C
A:Note: this serum tripeptide is found to stimulate growth of some cell types and to inh

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 G 1

Search completed: May 2, 2006, 08:56:20
Job time : 15.5116 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.6047 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-32
Perfect score: 0
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	Nan	2	1 GWA_SEPOF	P83570 sepiia offic
2	0	Nan	3	1 GRWM_HUMAN	P01157 homo sapien
3	0	Nan	3	1 LUXE_VIBFI	P24272 vibrilo fisc
4	0	Nan	3	1 THYL_BOMOR	P62970 bombina ori
5	0	Nan	3	1 THYL_NORVI	P62971 notophthalm
6	0	Nan	3	1 THYL_PIG	P62968 sus scrofa
7	0	Nan	3	1 THYL_SHEEP	P62969 ovis aries
8	0	Nan	4	1 ACHI_ACHFU	P35904 achatina fu
9	0	Nan	4	1 DCML_PSECH	P19916 pseudomonas
10	0	Nan	4	1 EOSTI_HUMAN	P02731 homo sapien
11	0	Nan	4	1 FAR3_HIRME	P42562 hirudo medi
12	0	Nan	4	1 FAR4_HIRME	P42563 hirudo medi
13	0	Nan	4	1 FLRF_HELTI	P58705 anthopleura
14	0	Nan	4	1 FLRF_HELTI	P69138 helisoma tr
15	0	Nan	4	1 FLRF_HIRME	P69137 hirudo medi
16	0	Nan	4	1 FLRF_HIRME	P58707 anthopleura
17	0	Nan	4	1 FLRF_HELTI	P69148 helisoma tr
18	0	Nan	4	1 FMRF_HIRME	P69147 hirudo medi
19	0	Nan	4	1 FMRF_HIRME	P69145 macrocallis
20	0	Nan	4	1 FMRF_HIRME	P69146 nereis vire
21	0	Nan	4	1 FMRF_HIRME	P58706 anthopleura
22	0	Nan	4	1 FMRF_HIRME	P83568 sepiia offic
23	0	Nan	4	1 FMRF_HIRME	P58648 octopus min
24	0	Nan	4	1 FMRF_HIRME	P58649 octopus min
25	0	Nan	4	1 FMRF_HIRME	P84465 pandinus im
26	0	Nan	4	1 FMRF_HIRME	P84464 pandinus im
27	0	Nan	4	1 FMRF_HIRME	P01858 homo sapien
28	0	Nan	4	1 FMRF_HIRME	P36515 saccharomyc
29	0	Nan	4	1 FMRF_HIRME	Q16047 homo sapien
30	0	Nan	4	1 FMRF_HIRME	Q96A70 homo sapien
31	0	Nan	4	1 FMRF_HIRME	Q96A70 homo sapien

32	0	Nan	4	2 Q08433	rattus sp.
33	0	Nan	5	1 ALI14_CARMA	P81817 carcinus ma
34	0	Nan	5	1 AP21_EISFO	P84182 eisenia foe
35	0	Nan	5	1 BIOA_CITFR	P13071 citrobacter
36	0	Nan	5	1 BIOB_CITFR	P12997 citrobacter
37	0	Nan	5	1 BP7_BOTIN	P30425 bothrops in
38	0	Nan	5	1 E103_LITRU	P82099 litoria rub
39	0	Nan	5	1 E104_LITRU	P82100 litoria rub
40	0	Nan	5	1 FARP_ARTTR	P41853 artiopesthi
41	0	Nan	5	1 FARP_CHICK	P83308 gallus gall
42	0	Nan	5	1 MPJ4_JUNVI	P81826 juniperus v
43	0	Nan	5	1 PAP2_PARMA	P81864 pardachirus
44	0	Nan	5	1 PRCT_CARMA	P67857 carcinus ma
45	0	Nan	5	1 PRCT_LIMPO	P67858 limulus pol

ALIGNMENTS

RESULT 1
GWA_SEPOF STANDARD; PRT; 2 AA.
AC P83570;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide Gwa.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
peptide inhibiting the motility of the mature oviduct in the
cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity
targeting the distal oviduct. Inhibits the motility of the oviduct
by decreasing tonus, frequency and amplitude of contractions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=VALDI; RANGE=1-2; NOTE=Ref.1.
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use as long as its content is in no way modified and this statement is not
removed.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 2 Tryptophan amide.
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000000 CRC64;
Query Match Nan%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 G 1
RESULT 2
GRWM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-modulating peptide.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=77162369; PubMed=858356;
 RA Schlesinger D.H., Pickart L., Thaler M.M.;
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
 RL Experientia 33:324-325(1977).
 CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
 CC growth of some cell types and to inhibit other types in vitro.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC GO; GO:0001558; P:regulation of cell growth; NAS.
 KW Direct protein sequencing.
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

 Query Match NaN%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 X 1
 DB 1 G 1

 RESULT 3
 LUXE VIBFI
 ID LUXE VIBFI STANDARD; PRT; 3 AA.
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
 DE protein synthetase) (Fragment).
 DE Name=luxE;
 GN Vibrio fischeri.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=668;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=91072226; PubMed=2254256;
 RA Swartzman E., Kapoor S., Graham A.P., Meighen E.A.;
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
 RT site for the lux operon".
 RL J. Bacteriol. 172:6797-6802(1990).
 CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
 CC is a component of the fatty acid reductase complex responsible for
 CC converting tetradecanoic acid to the aldehyde which serves as
 CC substrate in the luciferase-catalyzed reaction.
 CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -!- SIMILARITY: Belongs to the luxE family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M62812; -; NOT ANNOTATED_CDS; Genomic_DNA.
 KW Ligase; Luminescence.
 FT NON_TER 1
 SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match NaN%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 X 1
 DB 1 I 1

 RESULT 4
 THYL_BOMOR
 ID THYL_BOMOR STANDARD; PRT; 3 AA.
 AC P62970; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin-releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 OS Bombina orientalis (Oriental fire-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=8346;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR; A90919; RHDTFO.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

 Query Match NaN%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 X 1
 DB 1 Q 1

 RESULT 5
 THYL NOTVI
 ID THYL NOTVI STANDARD; PRT; 3 AA.
 AC P62971; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Thyroliberin (Thyrotropin-releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 OS Nophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC Nophthalmus.
 OX NCBI_TaxID=8316;
 RN [1]
 RP PROTEIN SEQUENCE.


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GN Name=cutL;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OC NCBI_TaxID=290;
RN [1]
RP PROTEIN SEQUENCE.
MEDLINE=9055678; PubMed=2818128;
RX Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of Co dehydrogenase structural genes in
RT carboxydrotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 1 Cu(+) ion per subunit.
CC -!- COFACTOR: Binds 1 Mo(6+) ion per subunit.
CC -!- COFACTOR: Binds 1 molybdopterin cytosine dinucleotide (MCD) per
CC subunit.
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; PLO140; PLO140.
KW Direct protein sequencing; Molybdenum; Oxidoreductase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;
-----
Query Match NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 M 1
-----
RESULT 10
DCMS_PSECH STANDARD; PRT; 4 AA.
ID AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit S) (CO-DH S) (Fragment).
GN Name=cutS;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OC NCBI_TaxID=290;
RN [1]
RP PROTEIN SEQUENCE.
MEDLINE=9055678; PubMed=2818128;
RX Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of Co dehydrogenase structural genes in
RT carboxydrotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 2 Fe-2S clusters (By similarity).
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
CC -----
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CC -----

CC PIR: PL0146;

DR 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;

KW Oxidoreductase.

FT NON TER 4

SQ - SEQUENCE 4 AA; 420 MW; 6DD33DB6F0000000 CRC64;

Query Match NaN%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 2 A 2

RESULT 11

EOSI HUMAN

ID EOSI HUMAN STANDARD; PRT; 4 AA.

AC P02731;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Eosinophilic tetrapeptides.

OS Homo sapiens (Human)

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

CC Homo.

CC NCBI_TaxID=9606;

CC [1]

PROTEIN SEQUENCE.

RX MEDLINE=76078412; PubMed=1060093;

RA Goetzl E.J.; Austen K.F.;

RT "Purification and synthesis of eosinophilic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";

RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

CC -!- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

CC -----

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CC -----

CC DR GO:0006935; P:chemotaxis; IDA.

CC GO:0006955; P:immune response; IDA.

KW Direct protein sequencing.

FT VARIANT 1 1 V -> A (in other peptide).

FT /FTID=VAR 005201.

SQ SEQUENCE 4 AA; 390 MW; 6B03B862A0000000 CRC64;

Query Match NaN%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 3 S 3

RESULT 12

FAR3_HIRME

ID FAR3_HIRME STANDARD; PRT; 4 AA.

AC P42562;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRamide-like neuropeptide YMRP-amide.

OS Hirudo medicinalis (Medicinal leech).

CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;

CC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

CC NCBI_TaxID=6421;

CC [1]

PROTEIN SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;

RA Evans B.D.; Pohl J.; Kartsonis M.A.; Calabrese R.L.;

RT "Identification of Rfamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.

CC -----

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CC -----

CC KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match NaN%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Y 1

RESULT 13

FAR4_HIRME

ID FAR4_HIRME STANDARD; PRT; 4 AA.

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRamide-like neuropeptide YMRP-amide.

OS Hirudo medicinalis (Medicinal leech)

CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;

CC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

CC NCBI_TaxID=6421;

CC [1]

PROTEIN SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;

RA Evans B.D.; Pohl J.; Kartsonis M.A.; Calabrese R.L.;

RT "Identification of Rfamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.

CC -----

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CC -----

CC KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match NaN%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

```
Db 1 Y 1
RESULT 14
FFKA ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-Khamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92028952; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Khamide), a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Khamide and Antho-Riamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR PIR; J01273;
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Alanine amide.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;
Query Match NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 4 A 4
RESULT 15
FLRF HELTI STANDARD; PRT; 4 AA.
AC P69138; P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FLRFamide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
```

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RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."
RL Peptides 15:31-36(1994).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
Query Match NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 F 1
Search completed: May 2, 2006, 08:46:48
Job time : 92.6047 secs
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 22.6977 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-32
Perfect score: 0
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	Nan	1	1	US-07-820-154A-12
2	0	Nan	1	1	US-07-791-213D-24
3	0	Nan	1	1	US-07-791-213D-40
4	0	Nan	1	1	US-08-174-365A-57
5	0	Nan	1	1	US-07-789-913-23
6	0	Nan	1	1	US-07-789-913-25
7	0	Nan	1	1	US-08-049-794-23
8	0	Nan	1	1	US-08-049-794-25
9	0	Nan	1	1	US-08-433-037-12
10	0	Nan	1	1	US-08-448-606-4
11	0	Nan	1	1	US-07-869-933-16
12	0	Nan	1	1	US-08-293-150A-24
13	0	Nan	1	1	US-08-293-150A-40
14	0	Nan	1	1	US-08-496-847-23
15	0	Nan	1	1	US-08-496-847-25
16	0	Nan	1	1	US-08-742-774-23
17	0	Nan	1	1	US-08-742-774-25
18	0	Nan	1	1	US-08-675-354-23
19	0	Nan	1	1	US-08-675-354-25
20	0	Nan	1	1	US-08-097-554A-12
21	0	Nan	1	1	US-08-965-918-23
22	0	Nan	1	1	US-08-965-918-25
23	0	Nan	1	1	US-09-138-439-23
24	0	Nan	1	1	US-09-138-439-25
25	0	Nan	1	2	US-08-480-640A-12
26	0	Nan	1	2	US-08-613-400A-23
27	0	Nan	1	2	US-08-613-400A-25

28	0	Nan	1	2	US-08-801-092-10	Sequence 10, Appl
29	0	Nan	1	2	US-08-801-092-17	Sequence 17, Appl
30	0	Nan	1	2	US-08-801-092-24	Sequence 24, Appl
31	0	Nan	1	2	US-08-801-092-31	Sequence 31, Appl
32	0	Nan	1	2	US-08-801-092-38	Sequence 38, Appl
33	0	Nan	1	2	US-08-801-092-45	Sequence 45, Appl
34	0	Nan	1	2	US-09-298-017-23	Sequence 23, Appl
35	0	Nan	1	2	US-09-298-017-25	Sequence 25, Appl
36	0	Nan	1	2	US-08-295-802-12	Sequence 12, Appl
37	0	Nan	1	2	US-09-392-979A-23	Sequence 23, Appl
38	0	Nan	1	2	US-09-392-979A-25	Sequence 25, Appl
39	0	Nan	1	2	US-09-103-663-16	Sequence 16, Appl
40	0	Nan	1	2	US-08-488-237A-12	Sequence 12, Appl
41	0	Nan	1	2	US-09-117-927-5	Sequence 5, Appl
42	0	Nan	1	2	US-08-375-992A-12	Sequence 12, Appl
43	0	Nan	1	2	US-09-315-113-10	Sequence 10, Appl
44	0	Nan	1	2	US-09-315-113-17	Sequence 17, Appl
45	0	Nan	1	2	US-09-315-113-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-07-820-154A-12
; Sequence 12, Application US/07820154A
; Patent No. 5382425
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Junker M.S., David E
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,154A
; FILING DATE: 19920113
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9850
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-820-154A-12

Query Match Nan%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 X 1

Db 1 V 1

RESULT 2
US-07-791-213D-24

Sequence 24, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-24

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 C 1

RESULT 3
US-07-791-213D-40
Sequence 40, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States

ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-40

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 C 1

RESULT 4
US-08-174-365A-57
Sequence 57, Application US/08174365A
Patent No. 5478809
GENERAL INFORMATION:
APPLICANT: Seichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,365A
FILING DATE: December 28, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 1 amino acid

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE: modified site

NAME/KEY: modified site

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note = "Xaa is modified amino acid as

OTHER INFORMATION: described in specification"

US-08-174-365A-57

Query Match

Best Local Similarity 100.0%; DB 1; Length 1;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 X 1

RESULT 5

US-07-789-913-23

Sequence 23, Application US/07789913

Patent No: 5559095

GENERAL INFORMATION:

APPLICANT: Miljanich, George P.

APPLICANT: Bowersox, Stephen S.

APPLICANT: Fox, James A.

APPLICANT: Valentino, Karen L.

APPLICANT: Bitner, Robert S.

APPLICANT: Yamashiro, Donald H.

TITLE OF INVENTION: Delayed Treatment Method of Reducing

TITLE OF INVENTION: Ischemia-Related Neuronal Damage

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Peter Dehlinger

STREET: 350 Cambridge Avenue, Suite 300

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/789,913

FILING DATE: 19911112

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/561,766

FILING DATE: 02-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/440,094

FILING DATE: 22-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0005.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 1 amino acids

TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: peptide fragment used in the claims

US-07-789-913-23

Query Match

Best Local Similarity 100.0%; DB 1; Length 1;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 C 1

RESULT 6

US-07-789-913-25

Sequence 25, Application US/07789913

Patent No: 5559095

GENERAL INFORMATION:

APPLICANT: Miljanich, George P.

APPLICANT: Bowersox, Stephen S.

APPLICANT: Fox, James A.

APPLICANT: Valentino, Karen L.

APPLICANT: Bitner, Robert S.

APPLICANT: Yamashiro, Donald H.

TITLE OF INVENTION: Delayed Treatment Method of Reducing

TITLE OF INVENTION: Ischemia-Related Neuronal Damage

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Peter Dehlinger

STREET: 350 Cambridge Avenue, Suite 300

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/789,913

FILING DATE: 19911112

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/561,766

FILING DATE: 02-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/440,094

FILING DATE: 22-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0005.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1 amino acids

TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: peptide fragment used in the claims

US-07-789-913-25

Query Match

Best Local Similarity 100.0%; DB 1; Length 1;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 7

US-08-049-794-23
; Sequence 23, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; NAME: Stratford, Carol A.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
; INDIVIDUAL ISOLATE: 32
US-08-049-794-23

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 C 1

RESULT 8

US-08-049-794-25
; Sequence 25, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L

APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; NAME: Stratford, Carol A.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
; INDIVIDUAL ISOLATE: 32
US-08-049-794-25

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 R 1

RESULT 9

US-08-433-037-12
; Sequence 12, Application US/08433037
; Patent No. 5707828
; GENERAL INFORMATION:
; APPLICANT: Sreekrishna, Kotikanyadan
; APPLICANT: Barr, Kathryn A.
; APPLICANT: Brierley, Russell A.
; APPLICANT: Thill, Gregory P.
; APPLICANT: Tschopp, Juerg F.
; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
; TITLE OF INVENTION: PICHIA PASTORIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 91082
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-037-12

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 L 1

RESULT 10
US-08-448-606-4
; Sequence 4, Application US/08448606
; Patent No. 5721114
; GENERAL INFORMATION:
; APPLICANT: Abrahams n, Lars
; APPLICANT: Holmgren, Erik
; APPLICANT: Kalder n, Christina
; APPLICANT: Lake, Mats
; APPLICANT: Mikaelsson, sa
; APPLICANT: Sejlitz, Torsten
; TITLE OF INVENTION: Expression System For Producing
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pollock, Vande Sande & Priddy
; STREET: 1990 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,606
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE93/01061
; FILING DATE: 09-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203753-0
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Amernick, Burton A.
; REGISTRATION NUMBER: 24,852
; REFERENCE/DOCKET NUMBER: 0151/00121
; TELECOMMUNICATION INFORMATION:

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 L 1

RESULT 11
US-07-869-933-16
; Sequence 16, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-869-933-16

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 M 1

RESULT 12
US-08-293-150A-24
; Sequence 24, Application US/08293150A

Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshihiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/293,150A
FILING DATE: 13-NOV-1990
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-24

Query Match NaN; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 C 1

RESULT 13
US-08-293-150A-40
Sequence 40, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshihiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria

STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-40

Query Match NaN; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 C 1

RESULT 14
US-08-496-847-23
Sequence 23, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 R 1
Search completed: May 2, 2006, 08:58:26
Job time : 22.6977 secs

REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
US-08-496-847-23

Query Match NaN; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 15
US-08-496-847-25
Sequence 25, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS, FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
US-08-496-847-25

Query Match NaN; Score 0; DB 1; Length 1;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 74.4186 Seconds
(without alignments)
44.917 Million cell updates/sec

Title: US-10-046-922-32
Perfect score: 0
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap.*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	NAN	1	3	US-09-778-885-5
2	0	NAN	1	3	US-09-909-348-4
3	0	NAN	1	3	US-09-982-172-3
4	0	NAN	1	3	US-09-982-172-4
5	0	NAN	1	3	US-09-982-172-9
6	0	NAN	1	3	US-09-982-172-11
7	0	NAN	1	3	US-09-982-172-19
8	0	NAN	1	3	US-09-982-172-31
9	0	NAN	1	3	US-09-982-172-35
10	0	NAN	1	3	US-09-982-172-37
11	0	NAN	1	3	US-09-982-172-46
12	0	NAN	1	3	US-09-982-172-69
13	0	NAN	1	3	US-09-982-172-80
14	0	NAN	1	3	US-09-982-172-81
15	0	NAN	1	3	US-09-982-172-83
16	0	NAN	1	3	US-09-982-172-86
17	0	NAN	1	3	US-09-982-172-93
18	0	NAN	1	3	US-09-982-172-95
19	0	NAN	1	3	US-09-982-172-106
20	0	NAN	1	3	US-09-982-172-112
21	0	NAN	1	3	US-09-982-172-120
22	0	NAN	1	3	US-09-982-172-126
23	0	NAN	1	3	US-09-982-172-148
24	0	NAN	1	3	US-09-982-172-149
25	0	NAN	1	3	US-09-982-172-155
26	0	NAN	1	3	US-09-982-172-160
27	0	NAN	1	3	US-09-982-172-172

28	0	NAN	1	3	US-09-982-172-173	Sequence 173, App
29	0	NAN	1	3	US-09-982-172-175	Sequence 175, App
30	0	NAN	1	3	US-09-982-172-189	Sequence 189, App
31	0	NAN	1	3	US-09-982-172-190	Sequence 190, App
32	0	NAN	1	3	US-09-982-172-191	Sequence 191, App
33	0	NAN	1	3	US-09-982-172-195	Sequence 195, App
34	0	NAN	1	3	US-09-982-172-200	Sequence 200, App
35	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
36	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
37	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
38	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
39	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
40	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
41	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
42	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
43	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
44	0	NAN	1	3	US-09-982-172-211	Sequence 211, App
45	0	NAN	1	3	US-09-982-172-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-778-885-5

; Sequence 5, Application US/09778885
; Publication No. US20020039748A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR MAKING IT
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/778,885
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 09/320,095
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 60/087,032
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide motif
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,
; OTHER INFORMATION: Pro, Trp or Val
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Pro
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)
; OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp,
; OTHER INFORMATION: Tyr or Val
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,
; OTHER INFORMATION: Ser, Thr or Trp
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr
; OTHER INFORMATION: or Met
; NAME/KEY: VARIANT
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,
; OTHER INFORMATION: Met, Phe or Trp
; NAME/KEY: VARIANT
; LOCATION: (8)...(8)

OTHER INFORMATION: Xaa is Gly or Glu
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr
NAME/KEY: VARIANT
LOCATION: (11)...(11)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,
OTHER INFORMATION: Pro, Trp and Val
NAME/KEY: VARIANT
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
OTHER INFORMATION: and Ser
NAME/KEY: VARIANT
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, Thr
OTHER INFORMATION: or Trp
NAME/KEY: VARIANT
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His,
OTHER INFORMATION: Ser, Trp or Tyr
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His,
OTHER INFORMATION: Met, Trp or Tyr
NAME/KEY: VARIANT
LOCATION: (16)...(16)
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile
NAME/KEY: VARIANT
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu
NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
NAME/KEY: VARIANT
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa is Tyr or Phe
NAME/KEY: VARIANT
LOCATION: (20)...(20)
OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp
NAME/KEY: VARIANT
LOCATION: (21)...(21)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
NAME/KEY: VARIANT
LOCATION: (22)...(22)
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp
NAME/KEY: VARIANT
LOCATION: (23)...(23)
OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val
NAME/KEY: VARIANT
LOCATION: (24)...(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
NAME/KEY: VARIANT
LOCATION: (25)...(25)
OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Tyr, Tyr

US-09-778-885-5

Query Match Nan%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 V 1

RESULT 2
US-09-909-348-4
; Sequence 4, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet

; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: Of The No. US20020042373A1-Proteolytically Activated Thrombin F
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(14)
; OTHER INFORMATION: Xaa at position six is Glu or Gln
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or
US-09-909-348-4

Query Match Nan%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 V 1

RESULT 3
US-09-982-172-3
; Sequence 3, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENER
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-3

Query Match Nan%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 4
US-09-982-172-4
; Sequence 4, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENER
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172

;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-4

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 5
US-09-982-172-9
;; Sequence 9, Application US/09982172
;; Patent No. US20020137119A1
;; GENERAL INFORMATION:
;; APPLICANT: Emil Israel Katz
;; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
;; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
;; TITLE OF INVENTION: UTILIZING EACH
;; FILE REFERENCE: 01/22283
;; CURRENT APPLICATION NUMBER: US/09/982,172
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-9.

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 6
US-09-982-172-11
;; Sequence 11, Application US/09982172
;; Patent No. US20020137119A1
;; GENERAL INFORMATION:
;; APPLICANT: Emil Israel Katz
;; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
;; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
;; TITLE OF INVENTION: UTILIZING EACH
;; FILE REFERENCE: 01/22283
;; CURRENT APPLICATION NUMBER: US/09/982,172
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 11
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 7
US-09-982-172-19
;; Sequence 19, Application US/09982172
;; Patent No. US20020137119A1
;; GENERAL INFORMATION:
;; APPLICANT: Emil Israel Katz
;; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
;; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
;; TITLE OF INVENTION: UTILIZING EACH
;; FILE REFERENCE: 01/22283
;; CURRENT APPLICATION NUMBER: US/09/982,172
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 19
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-19

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 8
US-09-982-172-31
;; Sequence 31, Application US/09982172
;; Patent No. US20020137119A1
;; GENERAL INFORMATION:
;; APPLICANT: Emil Israel Katz
;; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
;; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
;; TITLE OF INVENTION: UTILIZING EACH
;; FILE REFERENCE: 01/22283
;; CURRENT APPLICATION NUMBER: US/09/982,172
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 31
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-31.

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 9
US-09-982-172-35

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; Sequence 35, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-35

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 R 1

RESULT 10
US-09-982-172-37
; Sequence 37, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-37

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 K 1

RESULT 11
US-09-982-172-46
; Sequence 46, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-46

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 K 1

RESULT 12
US-09-982-172-69
; Sequence 69, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-69

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 K 1

RESULT 13
US-09-982-172-80
; Sequence 80, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-80

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
DB      1 K 1
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 K 1

RESULT 14

US-09-982-172-81
; Sequence 81, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-81

Query Match NaN; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 15

US-09-982-172-83
; Sequence 83, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-83

Query Match NaN; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

Search completed: May 2, 2006, 09:32:39
Job time : 74.4186 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17 ; Search time 11.3488 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 0

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New.*
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12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pepl.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	NaN	1	11	US-11-078-256-279
2	0	NaN	1	11	US-11-050-857-1142
3	0	NaN	1	11	US-11-144-947-395
4	0	NaN	1	11	US-11-144-947-611
5	0	NaN	1	11	US-11-264-096-184
6	0	NaN	1	11	US-11-264-096-186
7	0	NaN	1	11	US-11-264-096-325
8	0	NaN	1	11	US-11-264-096-500
9	0	NaN	1	11	US-11-264-096-744
10	0	NaN	1	11	US-11-264-096-1045
11	0	NaN	1	11	US-11-264-096-1119
12	0	NaN	1	11	US-11-264-096-1546
13	0	NaN	2	9	US-10-877-961B-121
14	0	NaN	2	9	US-10-913-711B-22
15	0	NaN	2	9	US-10-509-095A-40
16	0	NaN	2	9	US-10-509-095A-46
17	0	NaN	2	9	US-10-971-359A-2
18	0	NaN	2	9	US-10-971-359A-3
19	0	NaN	2	9	US-10-496-845A-7
20	0	NaN	2	9	US-10-760-085-42
21	0	NaN	2	9	US-10-644-807-322

22	0	NaN	2	11	US-11-043-806-531	Sequence 531, Appl
23	0	NaN	2	11	US-11-149-015-9	Sequence 9, Appl
24	0	NaN	2	11	US-11-149-015-54	Sequence 54, Appl
25	0	NaN	2	11	US-11-148-262-1	Sequence 1, Appl
26	0	NaN	2	11	US-11-148-262-2	Sequence 2, Appl
27	0	NaN	2	11	US-11-148-262-3	Sequence 3, Appl
28	0	NaN	2	11	US-11-148-262-4	Sequence 4, Appl
29	0	NaN	2	11	US-11-148-262-5	Sequence 5, Appl
30	0	NaN	2	11	US-11-148-262-6	Sequence 6, Appl
31	0	NaN	2	11	US-11-148-262-8	Sequence 8, Appl
32	0	NaN	2	11	US-11-148-262-9	Sequence 9, Appl
33	0	NaN	2	11	US-11-148-262-10	Sequence 10, Appl
34	0	NaN	2	11	US-11-148-262-11	Sequence 11, Appl
35	0	NaN	2	11	US-11-148-262-12	Sequence 12, Appl
36	0	NaN	2	11	US-11-148-262-13	Sequence 13, Appl
37	0	NaN	2	11	US-11-148-266-1	Sequence 1, Appl
38	0	NaN	2	11	US-11-148-266-2	Sequence 2, Appl
39	0	NaN	2	11	US-11-148-266-3	Sequence 3, Appl
40	0	NaN	2	11	US-11-148-266-4	Sequence 4, Appl
41	0	NaN	2	11	US-11-148-266-5	Sequence 5, Appl
42	0	NaN	2	11	US-11-148-266-6	Sequence 6, Appl
43	0	NaN	2	11	US-11-148-266-8	Sequence 8, Appl
44	0	NaN	2	11	US-11-148-266-9	Sequence 9, Appl
45	0	NaN	2	11	US-11-148-266-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-11-078-256-279
; Sequence 279, Application US/11078256
; Publication No. US20060035814A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padmini
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: 03-223-US
; CURRENT APPLICATION NUMBER: US/11/078,256
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 279
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is (R)4-9
US-11-078-256-279

Query Match NaN%; Score 0; DB 11; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1
Db 1 X 1

RESULT 2

US-11-050-857-1142
; Sequence 1142, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:

APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 1847,1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 1142
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-050-857-1142

Query Match NaN%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 E 1

RESULT 3
US-11-144-947-395
; Sequence 395, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0

US-11-144-947-395
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 395
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-947-395

Query Match NaN%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 M 1

RESULT 4

US-11-144-947-611
; Sequence 611, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0

US-11-144-947-611
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0

Query Match NaN%; Score 0; DB 11; Length 1;
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 M 1

RESULT 5
US-11-264-096-184
; Sequence 184, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 184
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-184

Query Match NaN; Score 0; DB 11; Length 1;
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 S 1

RESULT 6
US-11-264-096-186
; Sequence 186, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-186

Query Match NaN; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 S 1

RESULT 7
US-11-264-096-325
; Sequence 325, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 325
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-325

Query Match NaN; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 I 1

RESULT 8
US-11-264-096-500
; Sequence 500, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-500

Query Match NaN; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 M 1

RESULT 9
US-11-264-096-744
; Sequence 744, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 744
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-744

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

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Db      1 N 1

RESULT 10
US-11-264-096-1045
; Sequence 1045, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1045
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1045

Query Match      NaN%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 X 1
Db      1 C 1

RESULT 11
US-11-264-096-1119
; Sequence 1119, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1119
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1119

Query Match      NaN%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 X 1
Db      1 A 1

RESULT 12
US-11-264-096-1546
; Sequence 1546, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1546
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1546

Query Match      NaN%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 X 1
Db      1 M 1

RESULT 13
US-10-877-961B-121
; Sequence 121, Application US/10877961B
; Publication No. US20060003941A1
; GENERAL INFORMATION:
; APPLICANT: CanBas Co., Ltd.
; APPLICANT: Kawabe, Takumi
; APPLICANT: Kobayashi, Hidetaka
; TITLE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS HAVING IMMUNE-MODULATING, ANTI-
; FILE REFERENCE: 087533-0309084
; CURRENT APPLICATION NUMBER: US/10/877,961B
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: PCT/IB2004/002591
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: 60/482,750
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic peptide
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Positions 1 to 2 are D-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa is D-Phenylalanine-2,3,4,5,6-F
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa is D-Cyclohexyl-alanine
US-10-877-961B-121
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Query Match      NaN%; Score 0; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 X 1
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Db      1 X 1

RESULT 14
US-10-913-711B-22
; Sequence 22, Application US/10913711B
; Publication No. US20060014157A1
; GENERAL INFORMATION:
; APPLICANT: CanBas Co., Ltd.
; APPLICANT: Kawabe, Takumi
; APPLICANT: Kobayashi, Hidetaka
; TITLE OF INVENTION: SENSITIVITY TEST TO PREDICT EFFICACY OF ANTI-CANCER THERAPIES
; FILE REFERENCE: 087533-0310448
; CURRENT APPLICATION NUMBER: US/10/913,711B
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: 60/494,022
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Positions 1 to 2 are D-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is D-Phenylalanine-2,3,4,5,6-F
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa is D-Cyclohexyl-alanine
US-10-913-711B-22

Query Match      NaN%; Score 0; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 X 1
      |
Db      1 X 1

RESULT 15
US-10-509-095A-40
; Sequence 40, Application US/10509095A
; Publication No. US20060036073A1
; GENERAL INFORMATION:
; APPLICANT: WINDISCH, MANFRED
; TITLE OF INVENTION: NEUTROPHIC AND NEUROPROTECTIVE PEPTIDES
; FILE REFERENCE: 4301-1117
; CURRENT APPLICATION NUMBER: US/10/509,095A
; CURRENT FILING DATE: 2004-09-28
; PRIOR APPLICATION NUMBER: PCT/AT03/00065
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: AT A 495/2002
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn ver. 3.3
; SEQ ID NO 40
; LENGTH: 2
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-509-095A-40

Query Match      NaN%; Score 0; DB 9; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
      |
Db      1 G 1

Search completed: May 2, 2006, 09:33:44
Job time : 11.3488 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 28.3721 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	14	1	US-08-727-688-23
2	18	100.0	167	2	US-09-252-991A-17897
3	18	100.0	191	2	US-09-252-991A-25365
4	18	100.0	438	2	US-09-252-991A-31307
5	18	100.0	777	2	US-09-270-767-44409
6	18	100.0	801	1	US-07-906-349A-6
7	18	100.0	1152	2	US-09-303-518D-195
8	18	100.0	1388	2	US-09-463-048A-6
9	18	100.0	1497	2	US-09-060-854B-2
10	18	100.0	1497	2	US-09-529-904-3
11	18	100.0	1917	2	US-09-627-650B-5
12	18	100.0	1917	2	US-09-436-063C-5
13	18	100.0	2616	2	US-09-303-518D-879
14	17	94.4	45	1	US-08-824-379-3
15	17	94.4	48	4	PCT-US96-01720-9
16	17	94.4	150	2	US-09-252-991A-31728
17	17	94.4	156	2	US-09-252-991A-20612
18	17	94.4	169	2	US-09-252-991A-20344
19	17	94.4	169	2	US-09-252-991A-24301
20	17	94.4	172	2	US-09-252-991A-23050
21	17	94.4	180	2	US-09-303-518D-603
22	17	94.4	191	2	US-09-252-991A-19331
23	17	94.4	200	2	US-09-252-991A-22497
24	17	94.4	204	2	US-09-252-991A-31049
25	17	94.4	222	2	US-09-252-991A-26487
26	17	94.4	229	2	US-09-252-991A-29247
27	17	94.4	243	2	US-09-252-991A-25814

28	17	94.4	281	2	US-09-252-991A-29199	Sequence 29199, A
29	17	94.4	314	2	US-09-252-991A-31368	Sequence 31368, A
30	17	94.4	341	1	US-08-209-521-11	Sequence 11, Appl
31	17	94.4	414	1	US-09-252-991A-25096	Sequence 25096, A
32	17	94.4	684	2	US-09-303-518D-721	Sequence 721, Appl
33	17	94.4	908	2	US-08-714-741-44	Sequence 44, Appl
34	17	94.4	1400	2	US-08-630-915A-37	Sequence 37, Appl
35	17	94.4	1400	2	US-09-879-957-37	Sequence 86, Appl
36	17	94.4	1461	2	US-10-142-231-86	Sequence 1, Appl
37	17	94.4	1652	2	US-09-627-650B-1	Sequence 1, Appl
38	17	94.4	1652	2	US-09-436-063C-1	Sequence 7, Appl
39	17	94.4	2508	2	US-09-627-650B-7	Sequence 7, Appl
40	17	94.4	2508	2	US-09-436-063C-7	Sequence 3, Appl
41	17	94.4	2544	2	US-09-627-650B-3	Sequence 2, Appl
42	17	94.4	2544	2	US-09-436-063C-3	Sequence 9, Appl
43	17	94.4	2601	2	US-09-627-650B-9	Sequence 9, Appl
44	17	94.4	2601	2	US-09-436-063C-9	Sequence 30, Appl
45	17	94.4	2732	2	US-09-086-436-30	

ALIGNMENTS

RESULT 1
US-08-727-688-23
; Sequence 23, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5919638e
; US-08-727-688-23

Query Match 100.0%; Score 18; DB 1; Length 14;
Best Local Similarity 20.0%; Pred. No. 0.21;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CXXXXXXXC 10

Db 3 C S S S S S S S S A C 12

RESULT 2

US-09-252-991A-17897

Sequence 17897, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17897

LENGTH: 167

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-17897

Query Match 100.0%; Score 18; DB 2; Length 167;

Best Local Similarity 20.0%; Pred. No. 0.35;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 60 CSTSTTTC 69

RESULT 3

US-09-252-991A-25365

Sequence 25365, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25365

LENGTH: 191

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25365

Query Match 100.0%; Score 18; DB 2; Length 191;

Best Local Similarity 20.0%; Pred. No. 0.36;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 49 CSTAASATSC 58

RESULT 4

US-09-252-991A-31307

Sequence 31307, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31307

LENGTH: 438

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31307

Query Match 100.0%; Score 18; DB 2; Length 438;

Best Local Similarity 20.0%; Pred. No. 0.43;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 56 CSAATASSTC 65

RESULT 5

US-09-270-767-44409

Sequence 44409, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 44409

LENGTH: 777

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-44409

Query Match 100.0%; Score 18; DB 2; Length 777;

Best Local Similarity 20.0%; Pred. No. 0.48;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 729 CSTSSSSSSC 738

RESULT 6

US-07-906-349A-6

Sequence 6, Application US/07906349A

Patent No. 5434064

GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph

APPLICANT: Skolnik, Edward Y.

APPLICANT: Margolis, Benjamin L.

TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR

TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES

TITLE OF INVENTION: TARGET PROTEINS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,349A
FILING DATE: 30-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/643,237
FILING DATE: 18-JAN-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 801 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-906-349A-6

Query Match 100.0%; Score 18; DB 1; Length 801;
Best Local Similarity 20.0%; Pred. No. 0.48;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 608 CTTTTTTTC 617

RESULT 7
US-09-303-518D-195
Sequence 195, Application US/09303518D
Patent No. 6914131
GENERAL INFORMATION:
APPLICANT: Scarlato, Vincenzo
APPLICANT: Masignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisserial Antigens
FILE REFERENCE: CHIR0160
CURRENT APPLICATION NUMBER: US/09/303,518D
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 1098
SOFTWARE: PatentIn version 3.1
SEQ ID NO 195
LENGTH: 1152
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-09-303-518D-195

Query Match 100.0%; Score 18; DB 2; Length 1152;
Best Local Similarity 20.0%; Pred. No. 0.52;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1138 CAAAAAATAC 1147

RESULT 8
US-09-463-048A-6
Sequence 6, Application US/09463048A
Patent No. 6630619
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Research Organisation
APPLICANT: EAST, Peter David
TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photob
TITLE OF INVENTION: luminescens
FILE REFERENCE: 050179-0076
CURRENT APPLICATION NUMBER: US/09/463,048A

CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: PCI/AU98/00562
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: PO 8088
PRIOR FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 1388
TYPE: PRT
ORGANISM: Photorhabdus luminescens
US-09-463-048A-6

Query Match 100.0%; Score 18; DB 2; Length 1388;
Best Local Similarity 20.0%; Pred. No. 0.53;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 8 CTAATAATTC 17

RESULT 9
US-09-060-854B-2
Sequence 2, Application US/09060854B
Patent No. 6642011
GENERAL INFORMATION:
APPLICANT: Estell, David Aaron
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011
TITLE OF INVENTION: Proteins
FILE REFERENCE: GCS32
CURRENT APPLICATION NUMBER: US/09/060,854B
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1497
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-060-854B-2

Query Match 100.0%; Score 18; DB 2; Length 1497;
Best Local Similarity 20.0%; Pred. No. 0.54;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 30 CAATTAATAC 39

RESULT 10
US-09-529-904-3
Sequence 3, Application US/09529904
Patent No. 6831053
GENERAL INFORMATION:
APPLICANT: Ghosh, Chanchal K.
APPLICANT: Baeck, Andre C.
APPLICANT: Ohtani, Ryohai (nmn)
APPLICANT: Busch, Alfred (nmn)
APPLICANT: Showell, Michael S.
APPLICANT: Poullose, Ayrookaran J. (nmn)
APPLICANT: Schellenberger, Volker
APPLICANT: Kellis, Jr., James T.
APPLICANT: Paech, Christian (nmn)
APPLICANT: Nadherny, Joanne (nmn)
APPLICANT: Naki, Donald P.
APPLICANT: Collier, Katherine D.
APPLICANT: Caldwell, Robert M.
TITLE OF INVENTION: Bleaching compositions comprising multiply-substituted
TITLE OF INVENTION: protease variants
FILE REFERENCE: Bleaching comp comprising multiply-sub
CURRENT APPLICATION NUMBER: US/09/529,904

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; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 08/956,323
; PRIOR FILING DATE: 1997-10-23
; PRIOR APPLICATION NUMBER: US 08/956,564
; PRIOR FILING DATE: 1997-10-23
; PRIOR APPLICATION NUMBER: US 08/956,324
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-529-904-3

Query Match          100.0%; Score 18; DB 2; Length 1497;
Best Local Similarity 20.0%; Pred. No. 0.54;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      30 CAATTAATAC 39

RESULT 11
US-09-627-650B-5
; Sequence 5, Application US/09627650B
; Patent No. 6406872
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematoide Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 21101.000903
; CURRENT APPLICATION NUMBER: US/09/627,650B
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/436,063
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107,727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-627-650B-5

Query Match          100.0%; Score 18; DB 2; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.57;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      1049 CAATATATC 1058

RESULT 12
US-09-436-063C-5
; Sequence 5, Application US/09436063C
; Patent No. 6407210
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematoide Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: P-1095corrected
; CURRENT APPLICATION NUMBER: US/09/436,063C
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-436-063C-5

Query Match          100.0%; Score 18; DB 2; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.57;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      1049 CAATATATC 1058

RESULT 13
US-09-303-518D-879
; Sequence 879, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 879
; LENGTH: 2616
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-879

Query Match          100.0%; Score 18; DB 2; Length 2616;
Best Local Similarity 20.0%; Pred. No. 0.61;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      876 CAATTAATAC 885

RESULT 14
US-08-824-379-3
; Sequence 3, Application US/08824379
; Patent No. 585801
; GENERAL INFORMATION:
; APPLICANT: Rao, A. Gururaj
; TITLE OF INVENTION: High Threonine Derivatives of
; TITLE OF INVENTION: Alpha-Hordothionin
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States of America
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,379
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/459,180
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/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Simon, Soma G.
/ REGISTRATION NUMBER: 37,444
/ REFERENCE/DOCKET NUMBER: 354-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 515-248-4896
/ TELEFAX: 515-248-4844
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-824-379-3

Query Match 94.4%; Score 17; DB 1; Length 45;
Best Local Similarity 20.0%; Pred. No. 1.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 16 CTTTATTTC 25

RESULT 15
PCT-US96-01720-9
; Sequence 9, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-01720-9

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Best Local Similarity 20.0%; Pred. No. 1.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 3 CGTTAAATC 12

Search completed: May 2, 2006, 08:58:25
Job time : 28.3721 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 112.791 Seconds
(without alignments)

38.955 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	30	9	ADZ47471 Alu sense
2	18	100.0	89	8	ADP30533 Human sec
3	18	100.0	89	8	ADP30531 Human sec
4	18	100.0	109	4	AAW93527 Human pol
5	18	100.0	109	8	ADL31230 Human pro
6	18	100.0	109	8	ADP30690 Human sec
7	18	100.0	144	8	ADP31474 Human sec
8	18	100.0	167	7	ABO69151 Pseudomon
9	18	100.0	169	8	ADL12185 Human the
10	18	100.0	171	8	ADP30794 Human sec
11	18	100.0	171	8	ADP30793 Human sec
12	18	100.0	183	8	ADP30806 Human sec
13	18	100.0	191	7	ABO76619 Pseudomon
14	18	100.0	214	9	ADZ56213 Human KIA
15	18	100.0	228	8	ADP30921 Human sec
16	18	100.0	252	8	ADP31485 Human sec
17	18	100.0	258	8	ADP30479 Human sec
18	18	100.0	264	8	ADP31412 Human sec
19	18	100.0	270	8	ADP30500 Human sec
20	18	100.0	270	8	ADP31321 Human sec
21	18	100.0	294	8	ADP31473 Human sec
22	18	100.0	297	8	ADP31192 Human sec
23	18	100.0	328	4	AAW25285 Human pro
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25	18	100.0	348	8	ADP31441 Human sec
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28	18	100.0	357	8	ADP30505 Human sec
29	18	100.0	360	8	ADP31439 Human sec
30	18	100.0	390	8	ADP31218 Human sec
31	18	100.0	421	8	ADP31159 Human sec
32	18	100.0	426	8	ADP311495 Human sec
33	18	100.0	438	7	ABO82561 Pseudomon
34	18	100.0	453	8	ADP311465 Human sec
35	18	100.0	471	8	ADP30854 Human sec
36	18	100.0	525	8	ADP31227 Human sec
37	18	100.0	549	8	ADP30855 Human sec
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40	18	100.0	591	9	ADZ56209 Human KIA
41	18	100.0	591	9	ADZ56223 Human KIA
42	18	100.0	600	8	ADP30865 Human sec
43	18	100.0	604	8	ADP30940 Human sec
44	18	100.0	604	8	ADP30941 Human sec
45	18	100.0	604	8	ADP30941 Human sec

ALIGNMENTS

RESULT 1
ADZ47471
ID ADZ47471 standard; peptide; 30 AA.
XX ADZ47471;
XX
DT 30-JUN-2005 (first entry)
XX
DE Alu sense peptide SEQ ID NO 50.
XX
KW hyaluronan synthase; HAS; hyaluronidase; HYAL; HAS1; HAS2; HAS3; HYAL1;
KW HYAL2; HAL3; PH-20; cancer; hyperproliferation; inflammation; anabolic;
KW hypertensive; gynaecological; neuroprotective; anticancer; cytostatic;
KW anti-inflammatory; endocrine-gen; immunosuppressive; gene therapy.
XX Unidentified.
XX WO2005035548-A1.
XX
XX 21-APR-2005.
XX
XX 11-OCT-2004; 2004WO-AU001383.
XX
XX 10-OCT-2003; 2003AU-00905551.
XX 01-DEC-2003; 2003AU-00906658.
XX (MEDI-) MEDITECH RES LTD.
XX Brown TJ, Brownlee GR;
XX WPI; 2005-315540/32.
XX
XX Novel compound capable of reducing level, function or activity of
XX hyaluronan synthase or hyaluronidase, useful for treating cancer,
XX hyperproliferative condition, A-beta-lipoproteinemia, A-V, A beta-2-
XX microglobulin amyloidosis.
XX
XX Example 22; SEQ ID NO 50; 277pp; English.
XX
XX This invention describes a novel nucleic acid molecule capable of
XX reducing the level of hyaluronan synthase (HAS) or hyaluronidase (HYAL)
XX or the function or activity of HAS or HYAL. HAS is selected from HAS1,
XX HAS2 and HAS3. HYAL is chosen from HYAL1, HYAL2, HAL3 and PH-20. The
XX nucleic acid molecule is an oligonucleotide or its chemically modified
XX form comprising a chemically modified backbone or a non-natural
XX internucleoside linkage. The compound is an interactive molecule capable
XX of binding or otherwise associating with HAS and/or HYAL to reduce HAS

CC and/or HVAL function or activity. The novel molecule is useful for
 CC treating cancer, hyperproliferative conditions or inflammatory
 CC conditions. The products of the invention are useful for treating or
 CC prophylaxis of a condition in subject, which involves administering to
 CC the subject, an HAS and/or HVAL level-reducing or HAS and/or HVAL
 CC activity reducing effective amount of active molecule. The products of
 CC the invention have anabolic, hypertensive, gynaecological,
 CC neuroprotective, antianemic, cytostatic, anti-inflammatory, endocrine-
 CC gen. and immunosuppressive activity. This sequence represents a peptide
 CC used in the method of the invention. NOTE: The specification describes
 CC SEQ ID NO 27-51 as nucleotide primers however the Sequence Listing
 CC represents the nucleotides in a three letter amino acid code. The
 CC nucleotide sequences have been made and are represented in ().

XX SQ Sequence 30 AA;

Query Match 100.0%; Score 18; DB 9; Length 30;
 Best Local Similarity 20.0%; Pred. No. 2.4;
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
 |
 Db 18 CTAATAATAC 27

RESULT 2

ID ADP30533 standard; protein; 89 AA.

AC ADP30533;

DT 12-AUG-2004 (first entry)

XX Human secreted protein SEQ ID #1300.

DE Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
 KW cancer; inflammatory; immune; human secreted protein.

XX Homo sapiens.

XX WC2004035732-A2.

XX 29-APR-2004.

XX 28-AUG-2003; 2003WO-US026780.

XX 29-AUG-2002; 2002US-0406576P.

XX 29-AUG-2002; 2002US-0406579P.

XX 29-AUG-2002; 2002US-0406585P.

XX 29-AUG-2002; 2002US-0406588P.

XX 29-AUG-2002; 2002US-0406608P.

XX 29-AUG-2002; 2002US-0406611P.

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XX 29-AUG-2002; 2002US-0406616P.

XX 29-AUG-2002; 2002US-0406640P.

XX 29-AUG-2002; 2002US-0406642P.

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XX 29-AUG-2002; 2002US-0406655P.

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XX 17-SEP-2002; 2002US-0410979P.

XX 17-SEP-2002; 2002US-0410980P.

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XX 17-SEP-2002; 2002US-0411076P.

XX 17-SEP-2002; 2002US-0411077P.

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XX 17-SEP-2002; 2002US-0411107P.

XX 17-SEP-2002; 20

Db 24 CTTAAAAAAC 33

RESULT 3

ADP30531

ID ADP30531 standard; protein; 89 AA.

XX AC ADP30531;

XX DT 12-AUG-2004 (first entry)

XX DE Human secreted protein SEQ ID #1298.

XX DE Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;

XX DE cancer; inflammatory; immune; human secreted protein.

XX OS Homo sapiens.

XX PN WO2004035732-A2.

XX PD 29-APR-2004.

XX PF 28-AUG-2003; 2003WO-US026780.

XX PR 29-AUG-2002; 2002US-0406576P.

XX PR 29-AUG-2002; 2002US-0406579P.

XX PR 29-AUG-2002; 2002US-0406585P.

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XX PR 29-AUG-2002; 2002US-0406655P.

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XX PR 17-SEP-2002; 2002US-0410946P.

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XX PR 17-SEP-2002; 2002US-0411111P.

XX PR 18-APR-2003; 2003US-0463700P.

XX PR 18-APR-2003; 2003US-0463708P.

XX PR 18-APR-2003; 2003US-0463716P.

XX PR 18-APR-2003; 2003US-0463732P.

XX PR 02-MAY-2003; 2003US-0467199P.

XX PR 02-MAY-2003; 2003US-0467201P.

XX PR 02-MAY-2003; 2003US-0467203P.

02-MAY-2003; 2003US-0467230P.

19-MAY-2003; 2003US-0471306P.

19-MAY-2003; 2003US-0471338P.

22-MAY-2003; 2003US-0472420P.

22-MAY-2003; 2003US-0472430P.

09-JUN-2003; 2003US-0476609P.

09-JUN-2003; 2003US-0476641P.

08-JUL-2003; 2003US-0485218P.

08-JUL-2003; 2003US-0485223P.

08-JUL-2003; 2003US-0485224P.

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14-JUL-2003; 2003US-0486446P.

14-JUL-2003; 2003US-0486480P.

15-JUL-2003; 2003US-0486891P.

15-JUL-2003; 2003US-0486960P.

08-AUG-2003; 2003US-0493341P.

08-AUG-2003; 2003US-0493370P.

08-AUG-2003; 2003US-0493573P.

08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;

Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;

Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

WPI; 2004-348438/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases

such as proliferative (e.g. cancer), inflammatory, immune, metabolic,

genetic, bacterial and viral diseases.

Claim 1; SEQ ID NO 2529; 428pp; English.

The present invention relates to an isolated nucleic acid molecule

encoding a polypeptide which is believed to be cytostatic,

antiinflammatory, immunosuppressive, antibacterial and virucidal. The

composition and methods are useful for diagnosing, preventing and

treating diseases such as proliferative (e.g. cancer), inflammatory,

immune, metabolic, genetic, bacterial and viral diseases. The present

sequence represents a human secreted protein. The present sequence is

available on WIPOMEB and is not in the specification.

Sequence 89 AA;

Query Match 100.0%; Score 18; DB 8; Length 89;

Best Local Similarity 20.0%; Pred. No. 3.1;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Cy 1 CXXXXXXXC 10

Db 24 CTTAAAAAAC 33

RESULT 4

AAM93527

ID AAM93527 standard; protein; 109 AA.

XX AC AAM93527;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide; SEQ ID NO: 3263.

XX DE Human; full length cDNA; cDNA synthesis; oligo-capping.

XX OS Homo sapiens.

XX PN EP1130094-A2.

XX PD 05-SEP-2001.

XX PF 07-JUL-2000; 2000EP-00114089.

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XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
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XX XX
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX XX
XX DR WPI; 2001-524255/58.
XX DR N-PSDB; AAK94457.
XX XX
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX XX
XX PS Claim 8; SEQ ID NO 3263; 1380pp + Sequence Listing; English.
XX CC
XX CC The invention relates to primers for synthesizing full length cDNA
XX CC clones. 830 cDNA molecules encoding a human protein have been isolated
XX CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX CC been determined. Primers for synthesizing the full length cDNA are useful
XX CC for clarifying the function of the protein encoded by the cDNA. The full
XX CC length clones were obtained by construction of full length enriched cDNA
XX CC libraries that were synthesised by the oligo-capping method. The primers
XX CC enable the production of the full length cDNA easily without any special
XX CC methods. The present sequence is a polypeptide encoded by a full length
XX CC human cDNA of the invention. Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in CD-ROM
XX CC format directly from EPO
XX XX
XX SQ Sequence 109 AA;
XX Query Match 100.0%; Score 18; DB 4; Length 109;
XX Best Local Similarity 20.0%; Pred. No. 3.2;
XX Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 CXXXXXXXC 10
XX Db 4 CSSSATSTSC 13
XX
XX RESULT 5
XX ADL31230
XX ID ADL31230 standard; protein; 109 AA.
XX AC ADL31230;
XX XX
XX DT 20-MAY-2004 (first entry)
XX DE Human protein encoded by a full length cDNA clone SeqID 3263.
XX DE human; medicine; signal transduction; glycoprotein; transcription;
XX KW oligo-capping method.
XX KW
XX OS Homo sapiens.
XX XX
XX PN EP1396543-A2.
XX PD 10-MAR-2004.
XX PF 07-JUL-2000; 2003EP-00025638.
XX XX
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183865.
XX PR 07-JUL-2000; 2000EP-00114089.
XX XX
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX XX
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX XX
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DR WPI; 2004-204755/20.
DR N-PSDB; ADL31229.
XX PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX PT length human cDNAs.
XX PS Example 1; SEQ ID NO 3263; 1340pp; English.
XX CC
XX CC This invention relates to a novel primers useful for synthesising full
XX CC length cDNA molecules that encode human proteins. Specifically, it refers
XX CC to secretory or membrane proteins that are potential therapeutic agents/
XX CC target molecules in the field of medicine, and in particular genes
XX CC encoding proteins that are associated with signal transduction.
XX CC glycoproteins and transcription. The present invention describes a method
XX CC for efficiently cloning a full length human cDNA from both the 5' and 3'
XX CC ends using the oligo-capping method. This polypeptide sequence is a full
XX CC length human protein of the invention.
XX SQ Sequence 109 AA;
XX Query Match 100.0%; Score 18; DB 8; Length 109;
XX Best Local Similarity 20.0%; Pred. No. 3.2;
XX Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 CXXXXXXXC 10
XX Db 4 CSSSATSTSC 13
XX
XX RESULT 6
XX ADP30690
XX ID ADP30690 standard; protein; 109 AA.
XX AC ADP30690;
XX XX
XX DT 12-AUG-2004 (first entry)
XX DE Human secreted protein SEQ ID #1457.
XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
XX KW cancer; inflammatory; immune; human secreted protein.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO2004035732-A2.
XX PD 29-APR-2004.
XX PF 28-AUG-2003; 2003WO-US026780.
XX XX
XX PR 29-AUG-2002; 2002US-0406576P.
XX PR 29-AUG-2002; 2002US-0406579P.
XX PR 29-AUG-2002; 2002US-0406585P.
XX PR 29-AUG-2002; 2002US-0406588P.
XX PR 29-AUG-2002; 2002US-0406608P.
XX PR 29-AUG-2002; 2002US-0406611P.
XX PR 29-AUG-2002; 2002US-0406612P.
XX PR 29-AUG-2002; 2002US-0406616P.
XX PR 29-AUG-2002; 2002US-0406640P.
XX PR 29-AUG-2002; 2002US-0406642P.
XX PR 29-AUG-2002; 2002US-0406646P.
XX PR 29-AUG-2002; 2002US-0406653P.
XX PR 29-AUG-2002; 2002US-0406655P.
XX PR 29-AUG-2002; 2002US-0406666P.
XX PR 17-SEP-2002; 2002US-0410946P.
XX PR 17-SEP-2002; 2002US-0410947P.
XX PR 17-SEP-2002; 2002US-0410948P.
XX PR 17-SEP-2002; 2002US-0410949P.
XX PR 17-SEP-2002; 2002US-0410953P.
XX PR 17-SEP-2002; 2002US-0410957P.
XX PR 17-SEP-2002; 2002US-0410958P.
XX PR 17-SEP-2002; 2002US-0410959P.
XX PR 17-SEP-2002; 2002US-0410960P.
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PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang WM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX WPI; 2004-348438/32.
DR New nucleic acid molecule for diagnosing, preventing or treating diseases
XX such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
XX genetic, bacterial and viral diseases.
PS Claim 1; SEQ ID NO 3472; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPWEB and is not in the specification.
XX
XX Sequence 144 AA;
SQ
Query Match 100.0%; Score 18; DB 8; Length 144;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 CXXXXXXXXC 10
Db 72 CAATAAAATC 81
RESULT 8
ABO69151
ID ABO69151 standard; protein; 167 AA.
XX
XX ABO69151;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Pseudomonas aeruginosa polypeptide #1326.
DE
XX
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
KW
XX
XX Pseudomonas aeruginosa.
OS
XX
XX US6551795-B1.
PN
PR 12-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI
XX WPI; 2003-615309/58.
DR N-PSDB; ABD02722.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 17897; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 167 AA;
SQ
Query Match 100.0%; Score 18; DB 7; Length 167;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 CXXXXXXXXC 10
Db 60 CSTSTSTTSC 69
RESULT 9
ADS12185
ID ADS12185 standard; protein; 169 AA.
XX
XX ADS12185;
AC
XX
XX 16-DEC-2004 (first entry)
DT
XX
XX Human therapeutic contig.protein - SEQ ID 2422.
DE
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
PH
XX Misc-difference 1: 169
FT /label= Unknown, OTHER
FT /note= "OTHER = In-frame STOP codon"
XX
XX WO2004080148-A2.
PN
XX
XX 23-SEP-2004.
PD

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XX	30-SEP-2003; 2003WO-US030720.	XX	29-AUG-2002; 2002US-040655P.	XX	Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
XX	02-OCT-2002; 2002US-0416186P.	XX	29-AUG-2002; 2002US-040666P.	XX	Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
XX	(NUVE-) NUVELO INC.	XX	17-SEP-2002; 2002US-0410946P.	XX	Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX	Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;	XX	17-SEP-2002; 2002US-0410947P.	XX	WPI; 2004-348438/32.
XX	Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;	XX	17-SEP-2002; 2002US-0410948P.	XX	New nucleic acid molecule for diagnosing, preventing or treating diseases
XX	WPI; 2004-668857/65.	XX	17-SEP-2002; 2002US-0410949P.	XX	such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
XX	N-PSDB; ADS11587.	XX	17-SEP-2002; 2002US-0410953P.	XX	genetic, bacterial and viral diseases.
XX	New polynucleotide, useful in preparing a composition for diagnosing or	XX	17-SEP-2002; 2002US-0410957P.	XX	Claim 1; SEQ ID NO 2792; 428pp; English.
XX	treating inflammatory, neurodegenerative or stem cell disorders, e.g.,	XX	17-SEP-2002; 2002US-0410958P.	XX	The present invention relates to an isolated nucleic acid molecule
XX	aplastic anemia or cancer for promoting wound healing.	XX	17-SEP-2002; 2002US-0410960P.	XX	encoding a polypeptide which is believed to be cytostatic,
XX	Example 2; SEQ ID NO 2422; 718pp; English.	XX	17-SEP-2002; 2002US-0410961P.	XX	
XX	The invention relates to a novel isolated polynucleotide and the encoded	XX	17-SEP-2002; 2002US-0410962P.	XX	
XX	polypeptide. The molecules of the invention demonstrate antiinflammatory,	XX	17-SEP-2002; 2002US-0411041P.	XX	
XX	neuroprotective, antianemic, cytostatic and vulnerary activities and may	XX	17-SEP-2002; 2002US-0411045P.	XX	
XX	be useful in preparing a composition for diagnosing or treating	XX	17-SEP-2002; 2002US-0411046P.	XX	
XX	inflammatory, haematopoietic, immune, neurodegenerative or stem cell	XX	17-SEP-2002; 2002US-0411048P.	XX	
XX	disorders, such as aplastic anaemia or cancer, as well as for promoting	XX	17-SEP-2002; 2002US-0411052P.	XX	
XX	wound healing. The molecules may also be utilised during gene therapy	XX	17-SEP-2002; 2002US-0411055P.	XX	
XX	procedures. The current sequence is that of a human therapeutic contig	XX	17-SEP-2002; 2002US-0411073P.	XX	
XX	protein of the invention.	XX	17-SEP-2002; 2002US-0411082P.	XX	
XX	Sequence 169 AA;	XX	17-SEP-2002; 2002US-0411082P.	XX	
XX	Query Match 100.0%; Score 18; DB 8; Length 169;	XX	17-SEP-2002; 2002US-0411101P.	XX	
XX	Best Local Similarity. 20.0%; Pred. No. 3.5;	XX	17-SEP-2002; 2002US-0411111P.	XX	
XX	Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	XX	18-APR-2003; 2003US-0463700P.	XX	
QY	1 CXXXXXXXC 10	XX	18-APR-2003; 2003US-0463708P.	XX	
Db	81 CAAAAAAAC 90	XX	18-APR-2003; 2003US-0463716P.	XX	
RESULT 10		XX	18-APR-2003; 2003US-0463732P.	XX	
ID ADP30794		XX	02-MAY-2003; 2003US-0467199P.	XX	
ID ADP30794 standard; protein; 171 AA.		XX	02-MAY-2003; 2003US-0467201P.	XX	
ADP30794;		XX	02-MAY-2003; 2003US-0467203P.	XX	
XX		XX	02-MAY-2003; 2003US-0467203P.	XX	
XX		XX	19-MAY-2003; 2003US-0471306P.	XX	
12-AUG-2004 (first entry)		XX	19-MAY-2003; 2003US-0471338P.	XX	
Human secreted protein SEQ ID #1561.		XX	22-MAY-2003; 2003US-0472420P.	XX	
Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;		XX	22-MAY-2003; 2003US-0472430P.	XX	
cancer; inflammatory; immune; human secreted protein.		XX	09-JUN-2003; 2003US-0476609P.	XX	
Homo sapiens.		XX	09-JUN-2003; 2003US-0476641P.	XX	
WO2004035732-A2.		XX	08-JUL-2003; 2003US-0485218P.	XX	
29-APR-2004.		XX	08-JUL-2003; 2003US-0485223P.	XX	
28-AUG-2003; 2003WO-US026780.		XX	08-JUL-2003; 2003US-0485224P.	XX	
29-AUG-2002; 2002US-0406576P.		XX	08-JUL-2003; 2003US-0485325P.	XX	
29-AUG-2002; 2002US-0406579P.		XX	14-JUL-2003; 2003US-0486446P.	XX	
29-AUG-2002; 2002US-0406585P.		XX	14-JUL-2003; 2003US-0486480P.	XX	
29-AUG-2002; 2002US-0406588P.		XX	15-JUL-2003; 2003US-0486891P.	XX	
29-AUG-2002; 2002US-0406608P.		XX	15-JUL-2003; 2003US-0486960P.	XX	
29-AUG-2002; 2002US-0406611P.		XX	08-AUG-2003; 2003US-0493341P.	XX	
29-AUG-2002; 2002US-0406612P.		XX	08-AUG-2003; 2003US-0493370P.	XX	
29-AUG-2002; 2002US-0406616P.		XX	08-AUG-2003; 2003US-0493573P.	XX	
29-AUG-2002; 2002US-0406640P.		XX	08-AUG-2003; 2003US-0493577P.	XX	
29-AUG-2002; 2002US-					

CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
 CC composition and methods are useful for diagnosing, preventing and
 CC treating diseases such as proliferative (e.g. cancer), inflammatory,
 CC immune, metabolic, genetic, bacterial and viral diseases. The present
 CC sequence represents a human secreted protein. The present sequence is
 CC available on WIPWEB and is not in the specification.

XX SQ Sequence 171 AA;

Query Match 100.0%; Score 18; DB 8; Length 171;
 Best Local Similarity 20.0%; Pred. NO. 3.5;
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
 |
 Db 146 CAAATAAAC 155

RESULT 11

ADP30793
 ID ADP30793 standard; protein; 171 AA.

XX AC ADP30793;

XX DT 12-AUG-2004 (first entry)

XX DE Human secreted protein SEQ ID #1560.

XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
 cancer; inflammatory; immune; human secreted protein.

XX OS Homo sapiens.

XX PN WC2004035732-A2.

XX PD 29-APR-2004.

XX PF 28-AUG-2003; 2003WO-US026780.

XX PR 29-AUG-2002; 2002US-0406576P.

XX PR 29-AUG-2002; 2002US-0406579P.

XX PR 29-AUG-2002; 2002US-0406585P.

XX PR 29-AUG-2002; 2002US-0406588P.

XX PR 29-AUG-2002; 2002US-0406608P.

XX PR 29-AUG-2002; 2002US-0406611P.

XX PR 29-AUG-2002; 2002US-0406612P.

XX PR 29-AUG-2002; 2002US-0406616P.

XX PR 29-AUG-2002; 2002US-0406640P.

XX PR 29-AUG-2002; 2002US-0406642P.

XX PR 29-AUG-2002; 2002US-0406646P.

XX PR 29-AUG-2002; 2002US-0406653P.

XX PR 29-AUG-2002; 2002US-0406655P.

XX PR 29-AUG-2002; 2002US-0406666P.

XX PR 17-SEP-2002; 2002US-0410946P.

XX PR 17-SEP-2002; 2002US-0410947P.

XX PR 17-SEP-2002; 2002US-0410948P.

XX PR 17-SEP-2002; 2002US-0410949P.

XX PR 17-SEP-2002; 2002US-0410953P.

XX PR 17-SEP-2002; 2002US-0410957P.

XX PR 17-SEP-2002; 2002US-0410958P.

XX PR 17-SEP-2002; 2002US-0410959P.

XX PR 17-SEP-2002; 2002US-0410960P.

XX PR 17-SEP-2002; 2002US-0410961P.

XX PR 17-SEP-2002; 2002US-0410962P.

XX PR 17-SEP-2002; 2002US-0411019P.

XX PR 17-SEP-2002; 2002US-0411022P.

XX PR 17-SEP-2002; 2002US-0411023P.

XX PR 17-SEP-2002; 2002US-0411024P.

XX PR 17-SEP-2002; 2002US-0411032P.

XX PR 17-SEP-2002; 2002US-0411035P.

XX PR 17-SEP-2002; 2002US-0411037P.

XX PR 17-SEP-2002; 2002US-0411041P.

XX PR 17-SEP-2002; 2002US-0411045P.

PR 17-SEP-2002; 2002US-0411046P.
 PR 17-SEP-2002; 2002US-0411048P.
 PR 17-SEP-2002; 2002US-0411052P.
 PR 17-SEP-2002; 2002US-0411055P.
 PR 17-SEP-2002; 2002US-0411073P.
 PR 17-SEP-2002; 2002US-0411082P.
 PR 17-SEP-2002; 2002US-0411101P.
 PR 17-SEP-2002; 2002US-0411111P.
 PR 18-APR-2003; 2003US-0463700P.
 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463716P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 02-MAY-2003; 2003US-0467201P.
 PR 02-MAY-2003; 2003US-0467203P.
 PR 02-MAY-2003; 2003US-0467230P.
 PR 19-MAY-2003; 2003US-0471306P.
 PR 19-MAY-2003; 2003US-0471336P.
 PR 22-MAY-2003; 2003US-0472420P.
 PR 22-MAY-2003; 2003US-0472430P.
 PR 09-JUN-2003; 2003US-0476609P.
 PR 08-JUL-2003; 2003US-0476641P.
 PR 08-JUL-2003; 2003US-0485218P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 08-JUL-2003; 2003US-0485325P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 15-JUL-2003; 2003US-0486891P.
 PR 15-JUL-2003; 2003US-0486960P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493370P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;

Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;

Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

WPI; 2004-348438/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases
 such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
 genetic, bacterial and viral diseases.

Claim 1; SEQ ID NO 2791; 428pp; English.

The present invention relates to an isolated nucleic acid molecule
 encoding a polypeptide which is believed to be cytostatic,
 antiinflammatory, immunosuppressive, antibacterial and virucidal. The
 composition and methods are useful for diagnosing, preventing and
 treating diseases such as proliferative (e.g. cancer), inflammatory,
 immune, metabolic, genetic, bacterial and viral diseases. The present
 sequence represents a human secreted protein. The present sequence is
 available on WIPWEB and is not in the specification.

XX SQ Sequence 171 AA;

Query Match 100.0%; Score 18; DB 8; Length 171;

Best Local Similarity 20.0%; Pred. NO. 3.5;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 146 CAAATAAAC 155

RESULT 12

ADP30806

ID ADP30806 standard; protein; 183 AA.

XX

AC ADP30806;
 XX 12-AUG-2004 (first entry)
 DT Human secreted protein SEQ ID #1573.
 XX Cytostatic; Antinflammatory; Immunosuppressive; Antibacterial; Virucide;
 KW cancer; inflammatory; immune; human secreted protein.
 KW Homo sapiens.
 OS WO2004035732-A2.
 XX 29-APR-2004.
 XX 28-AUG-2003; 2003WO-US026780.
 XX 29-AUG-2002; 2002US-0406576P.
 XX 29-AUG-2002; 2002US-0406579P.
 XX 29-AUG-2002; 2002US-0406585P.
 XX 29-AUG-2002; 2002US-0406588P.
 XX 29-AUG-2002; 2002US-0406608P.
 XX 29-AUG-2002; 2002US-0406611P.
 XX 29-AUG-2002; 2002US-0406612P.
 XX 29-AUG-2002; 2002US-0406616P.
 XX 29-AUG-2002; 2002US-0406640P.
 XX 29-AUG-2002; 2002US-0406642P.
 XX 29-AUG-2002; 2002US-0406646P.
 XX 29-AUG-2002; 2002US-0406653P.
 XX 29-AUG-2002; 2002US-0406655P.
 XX 29-AUG-2002; 2002US-0406666P.
 XX 17-SEP-2002; 2002US-0410946P.
 XX 17-SEP-2002; 2002US-0410947P.
 XX 17-SEP-2002; 2002US-0410948P.
 XX 17-SEP-2002; 2002US-0410949P.
 XX 17-SEP-2002; 2002US-0410953P.
 XX 17-SEP-2002; 2002US-0410957P.
 XX 17-SEP-2002; 2002US-0410958P.
 XX 17-SEP-2002; 2002US-0410959P.
 XX 17-SEP-2002; 2002US-0410960P.
 XX 17-SEP-2002; 2002US-0410961P.
 XX 17-SEP-2002; 2002US-0410962P.
 XX 17-SEP-2002; 2002US-0411019P.
 XX 17-SEP-2002; 2002US-0411022P.
 XX 17-SEP-2002; 2002US-0411023P.
 XX 17-SEP-2002; 2002US-0411024P.
 XX 17-SEP-2002; 2002US-0411032P.
 XX 17-SEP-2002; 2002US-0411035P.
 XX 17-SEP-2002; 2002US-0411037P.
 XX 17-SEP-2002; 2002US-0411041P.
 XX 17-SEP-2002; 2002US-0411045P.
 XX 17-SEP-2002; 2002US-0411046P.
 XX 17-SEP-2002; 2002US-0411048P.
 XX 17-SEP-2002; 2002US-0411052P.
 XX 17-SEP-2002; 2002US-0411053P.
 XX 17-SEP-2002; 2002US-0411073P.
 XX 17-SEP-2002; 2002US-0411101P.
 XX 17-SEP-2002; 2002US-0411111P.
 XX 18-APR-2003; 2003US-0463700P.
 XX 18-APR-2003; 2003US-0463708P.
 XX 18-APR-2003; 2003US-0463716P.
 XX 18-APR-2003; 2003US-0463732P.
 XX 02-MAY-2003; 2003US-0467199P.
 XX 02-MAY-2003; 2003US-0467201P.
 XX 02-MAY-2003; 2003US-0467203P.
 XX 02-MAY-2003; 2003US-0467230P.
 XX 19-MAY-2003; 2003US-0471306P.
 XX 19-MAY-2003; 2003US-0471336P.
 XX 22-MAY-2003; 2003US-0472420P.
 XX 22-MAY-2003; 2003US-0472430P.
 XX 09-JUN-2003; 2003US-0476609P.
 XX 09-JUN-2003; 2003US-0476641P.
 PR 08-JUL-2003; 2003US-0485218P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 08-JUL-2003; 2003US-0485325P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 15-JUL-2003; 2003US-0486891P.
 PR 15-JUL-2003; 2003US-0486960P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493370P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.
 XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
 PA Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
 PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
 PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
 XX WPI; 2004-348438/32.
 XX New nucleic acid molecule for diagnosing, preventing or treating diseases
 PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
 PT genetic, bacterial and viral diseases.
 XX Claim 1; SEQ ID NO 2804; 428pp; English.
 PS The present invention relates to an isolated nucleic acid molecule
 CC encoding a polypeptide which is believed to be cytostatic,
 CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
 CC composition and methods are useful for diagnosing, preventing and
 CC treating diseases such as proliferative (e.g. cancer), inflammatory,
 CC immune, metabolic, genetic, bacterial and viral diseases. The present
 CC sequence represents a human secreted protein. The present sequence is
 CC available on WIPOWEB and is not in the specification.
 XX Sequence 183 AA;
 SQ Query Match 100.0%; Score 18; DB 8; Length 183;
 Best Local Similarity 20.0%; Pred.No. 3.6;
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 CXXXXXXXC 10
 DB 36 CATTTTTC 45
 RESULT 13
 ABO76619
 ID ABO76619 standard; protein; 191 AA.
 XX ABO76619;
 AC ABO76619;
 XX 29-JUL-2004 (first entry)
 DT Pseudomonas aeruginosa polypeptide #8794.
 XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX Pseudomonas aeruginosa.
 XX US6551795-B1.
 XX 22-APR-2003.
 XX 18-FEB-1999; 99US-00252991.
 XX 18-FEB-1998; 98US-0074788P.
 XX 27-JUL-1998; 98US-0094190P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 PI

```
XX DR WPI; 2003-615309/58.
XX DR N-PSDB; ABD10190.
XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX PS Disclosure; SEQ ID NO 25365; 455bp; English.
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-P. aeruginosa drugs, as templates for recombinant
XX CC production of P. aeruginosa-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of P. aeruginosa-caused
XX CC infection, and in detection of P. aeruginosa sequences or other sequences
XX CC of Pseudomonas species using biochip technology. Sequences ABO67826-
XX CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html
XX SQ Sequence 191 AA;
Query Match 100.0%; Score 18; DB 7; Length 191;
Best Local Similarity 20.0%; Pred. No. 3.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Oy 1 CXXXXXXXXC 10
Db 49 CSTAASATSC 58
RESULT 14
ADZ56213
ID ADZ56213 standard; protein; 214 AA.
XX AC ADZ56213;
XX DT 30-JUN-2005 (first entry)
XX DE Human KIAA0779 splice variant clone CLN00149041.a, protein.
XX KW KIAA0779; gene expression; inflammation; antiinflammatory; cancer;
XX KW proliferation; neoplasm; cytostatic; immune disorder; immunomodulator;
XX KW metabolic disorder; metabolic; viral infection; virucide; infection.
XX OS Homo sapiens.
XX PN WO2005035569-A2.
XX PD 21-APR-2005.
XX PF 12-OCT-2004; 2004WO-US033408.
XX PR 10-OCT-2003; 2003US-0510612P.
XX PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX PI Wong JGP, Hestir K, Collins ALT;
XX WPI; 2005-296268/30.
XX DR N-PSDB; ADZ56200, ADZ56231.
XX PT New isolated KIAA0779 nucleic acids and polypeptides, useful for
XX PT diagnosing, preventing and/or treating inflammatory, immune, viral
XX PT disorders and cancer, such as kidney, lung, ovarian, bladder, breast,
XX PT prostate and skin cancers.
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XX PS Claim 11; SEQ ID NO 18; 121pp; English.
XX CC The invention relates to an isolated nucleic acid molecule comprising at
XX CC least one polynucleotide sequence (appearing as ADZ56196-ADZ56197,
XX CC ADZ56199-ADZ56200, ADZ56226-ADZ56227 and ADZ56230-ADZ56231), sequences
XX CC hybridizing to them under high stringency conditions, sequences having at
XX CC least 80% sequence identity to them, their complements or biologically
XX CC active fragments. The nucleic acids are splice variants of the human
XX CC KIAA0779 gene, encoding transmembrane domain protein(s). Also included
XX CC are a double-stranded isolated nucleic acid molecule comprising the
XX CC nucleic acid molecule cited above, a vector comprising the isolated
XX CC nucleic acid molecule cited above, (and a promoter that regulates the
XX CC expression of the nucleic acid molecule), a recombinant host cell
XX CC comprising the nucleic acid molecule cited above, an isolated polypeptide
XX CC (comprising the encoded proteins or the non-transmembrane (TM) regions of
XX CC the proteins), a method of making a recombinant host cell, a method of
XX CC making a polypeptide, a method of determining the presence of the nucleic
XX CC acid molecule cited above in a sample, a method of determining the
XX CC presence of a specific antibody to the polypeptide of (4) in a sample, a
XX CC method of determining the presence of the polypeptide in a sample, an
XX CC antibody specifically binding to and/or interfering with the biological
XX CC activity of the nucleic acid molecule cited above (or the polypeptide or
XX CC its biologically active fragment), a composition comprising a
XX CC pharmaceutical carrier or excipient (and one or more active agents chosen
XX CC from the nucleic acid molecule cited above, the vector, the polypeptide,
XX CC and the antibody), a bacteriophage comprising the antibody (or its
XX CC fragment), a bacterial cell comprising the bacteriophage, a recombinant
XX CC host cell that produces from the nucleic acid molecule, the vector, the
XX CC active agents (chosen from the nucleic acid molecule, the vector, the
XX CC host cell, the polypeptide, and the antibody), a diagnostic kit
XX CC (comprising a nucleic acid molecule having at least 6 contiguous
XX CC nucleotides from the nucleic acid molecule cited above, the isolated
XX CC polypeptide, or antibody, and reagents to carry out an immunoassay), a
XX CC method of making an antibody, a method of identifying a modulating agent
XX CC that modulates the biological activity of the polypeptide, a modulator
XX CC composition comprising a modulator and a pharmaceutical carrier, a method
XX CC of treating a disease in a subject, and a method of treating cancer,
XX CC preferably kidney, cervical, squamous lung, ovarian, bladder, breast,
XX CC endometrial, prostate, and skin cancer, in a subject. The methods and
XX CC compositions of the present invention are useful for the diagnosis,
XX CC prevention and/or treatment of inflammatory, immune, viral disorders and
XX CC cancer, such as kidney, cervical, squamous lung, ovarian, bladder,
XX CC breast, endometrial, prostate, and skin cancer. The present sequence
XX CC represents a protein encoded by a cDNA splice variant from the KIAA0779
XX CC gene.
XX SQ Sequence 214 AA;
Query Match 100.0%; Score 18; DB 9; Length 214;
Best Local Similarity 20.0%; Pred. No. 3.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Oy 1 CXXXXXXXXC 10
Db 173 CAAAAAACC 182
RESULT 15
ADP30921
ID ADP30921 standard; protein; 228 AA.
XX AC ADP30921;
XX DT 12-AUG-2004 (first entry)
XX DE Human secreted protein SEQ ID #1688.
XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
XX KW cancer; inflammatory; immune; human secreted protein.
XX OS Homo sapiens.
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Tue May 2 12:32:37 2006

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PN WO2004035732-A2.
XX 29-APR-2004.
PD
XX 28-AUG-2003; 2003WO-US026780.
XX
XX 29-AUG-2002; 2002US-0406576P.
XX 29-AUG-2002; 2002US-0406579P.
XX 29-AUG-2002; 2002US-0406585P.
XX 29-AUG-2002; 2002US-0406588P.
XX 29-AUG-2002; 2002US-0406608P.
XX 29-AUG-2002; 2002US-0406611P.
XX 29-AUG-2002; 2002US-0406612P.
XX 29-AUG-2002; 2002US-0406616P.
XX 29-AUG-2002; 2002US-0406640P.
XX 29-AUG-2002; 2002US-0406642P.
XX 29-AUG-2002; 2002US-0406646P.
XX 29-AUG-2002; 2002US-0406653P.
XX 29-AUG-2002; 2002US-0406655P.
XX 29-AUG-2002; 2002US-0406666P.
XX 17-SEP-2002; 2002US-0410946P.
XX 17-SEP-2002; 2002US-0410947P.
XX 17-SEP-2002; 2002US-0410949P.
XX 17-SEP-2002; 2002US-0410953P.
XX 17-SEP-2002; 2002US-0410957P.
XX 17-SEP-2002; 2002US-0410958P.
XX 17-SEP-2002; 2002US-0410959P.
XX 17-SEP-2002; 2002US-0410960P.
XX 17-SEP-2002; 2002US-0410961P.
XX 17-SEP-2002; 2002US-0411019P.
XX 17-SEP-2002; 2002US-0411022P.
XX 17-SEP-2002; 2002US-0411023P.
XX 17-SEP-2002; 2002US-0411024P.
XX 17-SEP-2002; 2002US-0411032P.
XX 17-SEP-2002; 2002US-0411035P.
XX 17-SEP-2002; 2002US-0411037P.
XX 17-SEP-2002; 2002US-0411041P.
XX 17-SEP-2002; 2002US-0411045P.
XX 17-SEP-2002; 2002US-0411046P.
XX 17-SEP-2002; 2002US-0411048P.
XX 17-SEP-2002; 2002US-0411052P.
XX 17-SEP-2002; 2002US-0411055P.
XX 17-SEP-2002; 2002US-0411073P.
XX 17-SEP-2002; 2002US-0411082P.
XX 17-SEP-2002; 2002US-0411101P.
XX 17-SEP-2002; 2002US-0411111P.
XX 18-APR-2003; 2003US-0463700P.
XX 18-APR-2003; 2003US-0463708P.
XX 18-APR-2003; 2003US-0463716P.
XX 18-APR-2003; 2003US-0463732P.
XX 02-MAY-2003; 2003US-0467199P.
XX 02-MAY-2003; 2003US-0467201P.
XX 02-MAY-2003; 2003US-0467203P.
XX 02-MAY-2003; 2003US-0467230P.
XX 19-MAY-2003; 2003US-0471306P.
XX 19-MAY-2003; 2003US-0471336P.
XX 22-MAY-2003; 2003US-0472420P.
XX 22-MAY-2003; 2003US-0472430P.
XX 09-JUN-2003; 2003US-0476609P.
XX 09-JUN-2003; 2003US-0476641P.
XX 08-JUL-2003; 2003US-0485218P.
XX 08-JUL-2003; 2003US-0485223P.
XX 08-JUL-2003; 2003US-0485224P.
XX 08-JUL-2003; 2003US-0485325P.
XX 14-JUL-2003; 2003US-0486446P.
XX 14-JUL-2003; 2003US-0486480P.
XX 15-JUL-2003; 2003US-0486891P.
XX 15-JUL-2003; 2003US-0486960P.
XX 08-AUG-2003; 2003US-0493341P.
XX 08-AUG-2003; 2003US-0493370P.
XX 08-AUG-2003; 2003US-0493573P.

PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 2919; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
XX SQ Sequence 228 AA;
    Query Match 100.0%; Score 18; DB 8; Length 228;
    Best Local Similarity 20.0%; Pred. No. 3.8;
    Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
    Qy 1 CXXXXXXXC 10
    Db 54 CATAAATTAC 63

Search completed: May 2, 2006, 08:54:55
Job time : 113.791 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 18.1395 Seconds
(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	18	100.0	313	2 S59448	hypothetical prote
2	18	100.0	480	2 E75433	hypothetical prote
3	17	94.4	194	2 JQ1560	hypothetical 20.6K
4	17	94.4	220	2 JC4082	coat protein - Cym
5	17	94.4	376	2 AB2920	cobalamin biosynth
6	17	94.4	388	2 C97694	hypothetical prote
7	17	94.4	389	2 T33167	probable kexin (EC
8	17	94.4	570	2 T37314	dnak-type molecula
9	17	94.4	634	2 S33575	protein bli-4b [im
10	17	94.4	942	2 D87803	G surface protein
11	17	94.4	2704	2 S09118	hypothetical prote
12	16	88.9	71	2 E84312	hypothetical prote
13	16	88.9	85	2 E70531	hypothetical prote
14	16	88.9	104	2 S51479	drought-induced pr
15	16	88.9	105	2 A71249	hypothetical prote
16	16	88.9	108	2 F72549	hypothetical prote
17	16	88.9	126	2 A23473	chymotrypsin-like
18	16	88.9	129	2 T49498	hypothetical prote
19	16	88.9	133	2 A96745	hypothetical prote
20	16	88.9	147	2 S09762	hypothetical prote
21	16	88.9	153	2 PN0103	hypothetical 17K p
22	16	88.9	161	2 T28088	hypothetical prote
23	16	88.9	164	2 JQ1252	hypothetical 16.7K
24	16	88.9	229	2 T34277	hypothetical prote
25	16	88.9	242	2 A45724	pectate lyase (EC
26	16	88.9	244	2 S72219	chymotrypsin B - A
27	16	88.9	251	2 A55035	cysteine-rich prot
28	16	88.9	262	1 JQ1724	E1 membrane glycop
29	16	88.9	263	2 S47537	chymotrypsin (EC 3

30	16	88.9	275	2 A85856	probable elongatio
31	16	88.9	275	2 B64986	hypothetical 30.9
32	16	88.9	275	2 G91011	probable elongatio
33	16	88.9	294	2 T23682	hypothetical prote
34	16	88.9	306	2 C71498	probable yop trans
35	16	88.9	317	2 T00500	probable elicitor
36	16	88.9	321	2 A84792	hypothetical prote
37	16	88.9	349	2 JE0202	paired-box-contain
38	16	88.9	380	2 T04007	hypothetical prote
39	16	88.9	397	2 T26077	hypothetical prote
40	16	88.9	422	2 S41514	RAD52 protein homo
41	16	88.9	473	2 C81039	lipopolysaccharide
42	16	88.9	473	2 C81984	probable lipopolys
43	16	88.9	475	2 T36342	probable glutamate
44	16	88.9	486	2 B86460	hypothetical prote
45	16	88.9	510	2 A55207	glycerol-3-phospha

ALIGNMENTS

RESULT 1
S59448
hypothetical protein YMR206w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YMB325.07
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S59448
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59441
A;Accession: S59448
A;Molecule type: DNA
A;Residues: 1-313 <ODE>
A;Cross-references: UNIPROT:Q03695; UNIPARC:UPI000013B90A; EMBL.Z48755; NID:G736296; P
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YMR206w
A;Cross-references: SGD:S0004819
A;Map position: 13R

Query Match 100.0%; Score 18; DB 2; Length 313;
Best Local Similarity 20.0%; Pred. No. 0.44;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 245 CSSSSSSSSAC 254

RESULT 2
E75433
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75433
R;White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75433
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <WHI>
A;Cross-references: UNIPROT:Q9RV87; UNIPARC:UPI000000C18A8; GB:AE001963; GB:AE000513; P
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1142
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR1142

A.; Authors: Yoo, H.; Tao, Y.; Blade, F.; Jung, M.; Krespan, W.; Kelly, M.; Gordon-Kamm, A.; Author: Yoo, H.; Tao, Y.; Blade, F.; Jung, M.; Krespan, W.; Kelly, M.; Score 94.4%; DB 2; Length 389; Query Match

A;Description: involved in protein folding and assembling/disassembling of protein com
C;Superfamily: bcr protein
C;Keywords: ATP; mitochondrion; molecular chaperone; stress-induced protein
F;1-23/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;24-634/Product: heat shock protein 70, mitochondrial #status predicted <MAT>

Query Match 94.4%; Score 17; DB 2; Length 634;
Best Local Similarity 20.0%; Pred. No. 2.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 7 CGSAAASAC 16

RESULT 10
D87803
protein bli-4D [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-2002
C;Accession: D87803
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol.
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_e
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a
A;Accession: D87803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-942 <STO>
A;Cross-references: UNIPARC:UPI000016B639; GB:chr_I; PIDN:AAB96754.1; PID:g2773243; GS
C;Genetics:
A;Map position: 1
A;Gene: bli-4D
C;Superfamily: kexin; subtilisin homology

Query Match 94.4%; Score 17; DB 2; Length 942;
Best Local Similarity 20.0%; Pred. No. 2.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 683 CTESSSATSC 692

RESULT 11
S09118
G surface protein 168 - Paramesicium primaurelia
C;Species: Paramesicium primaurelia
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S09118
R;Prat, A.
J. Mol. Biol. 211, 521-535, 1990
A;Title: Conserved sequences flank variable tandem repeats in two alleles of the G sur
A;Reference number: S09118; MUID:90172419; PMID:2308165
A;Accession: S09118
A;Molecule type: DNA
A;Residues: 1-2704 <PRA>
A;Cross-references: UNIPROT:P17053; UNIPARC:UPI000012AE23; EMBL:X52133; NID:g10049; PI
C;Genetics:
A;Genetic code: SGC5
C;Superfamily: G surface protein

Query Match 94.4%; Score 17; DB 2; Length 2704;
Best Local Similarity 20.0%; Pred. No. 4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 1632 CVAATATTC 1641

probable kexin (EC 3.4.21.61) - Caenorhabditis elegans (fragment)
N;Alternate names: blisterase 4
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T37314
R;Thacker, C.; Peters, K.; Srayko, M.; Rose, A.M.
Genes Dev. 9, 956-971, 1995
A;Title: The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/su
A;Reference number: 221679; MUID:95293228; PMID:7774813
A;Accession: T37314
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-570 <THA>
A;Cross-references: UNIPARC:UPI000016B8E1; EMBL:L29440; NID:g459702; PIDN:AAA98752.1; PI
C;Genetics:
A;Gene: bli-4
A;Map position: 1
C;Keywords: alternative splicing; hydrolase; serine proteinase

Query Match 94.4%; Score 17; DB 2; Length 570;
Best Local Similarity 20.0%; Pred. No. 2.3;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 311 CTESSSATSC 320

RESULT 9
S33575
dnak-type molecular chaperone precursor, mitochondrial - Leishmania major
N;Alternate names: heat shock protein 70-related protein; mitochondrial stress protein
C;Species: Leishmania major
C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 31-Dec-2004
C;Accession: S33575; S78090; S05438
R;Searle, S.; McCrossan, M.V.; Smith, D.F.
J. Cell Sci. 104, 1091-1100, 1993
A;Title: Expression of a mitochondrial stress protein in the protozoan parasite Leishman
A;Reference number: S33575; MUID:93300981; PMID:8314893
A;Accession: S33575
A;Molecule type: DNA
A;Residues: 1-634 <SEA>
A;Cross-references: UNIPROT:P12076; UNIPARC:UPI0000177D24; EMBL:X64137
R;Smith, D.F.
submitted to the EMBL Data Library, January 1992
A;Reference number: S78090
A;Accession: S78090
A;Molecule type: DNA
A;Residues: 1-460,481-500, 'QGERIAENQIRGFDSG', 501-634 <SMI>
A;Cross-references: UNIPARC:UPI000012CC5C; EMBL:X64137; NID:g311289; PIDN:CAA45498.1; PI
R;Searle, S.; Campos, A.J.R.; Coulson, R.M.R.; Spithill, T.W.; Smith, D.F.
Nucleic Acids Res. 17, 5081-5095, 1989
A;Title: A family of heat shock protein 70-related genes are expressed in the promastig
A;Reference number: S05438; MUID:89345072; PMID:2762121
A;Accession: S05438
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <SEF>
A;Cross-references: UNIPARC:UPI000016BF1C; EMBL:X14574; NID:g9561; PIDN:CAA32713.1; PID:
C;Genetics:
A;Gene: Lmshp70.1
A;Genome: nuclear
C;Function:

RESULT 12

F84312
hypothetical protein Vng1598h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84312
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabcobson, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: F84312
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <STO>
A:Cross-references: UNIPROT:Q9HPK1; UNIPARC:UPI0000063920; GB:AE004437; NID:g10581076; F84312
C:Genetics:
A:Gene: VNG1598H

Query Match 88.9%; Score 16; DB 2; Length 71;
Best Local Similarity 20.0%; Pred. No. 4.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
DB 30 CSRSVSTSTC 39

RESULT 13

E70531
hypothetical protein Rv2706c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: E70531
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70531
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-85 <COL>
A:Cross-references: UNIPROT:O07207; UNIPARC:UPI000000C14DC; GB:Z96072; GB:AL123456; NID:g10581076
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv2706c

Query Match 88.9%; Score 16; DB 2; Length 85;
Best Local Similarity 20.0%; Pred. No. 5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
DB 24 CSATAVAACV 33

RESULT 14

S51479
drought-induced protein Di21 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 15-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S51479; S43176
R;Gosti, F.; Bertauche, N.; Vartanian, N.; Giraudat, J.
Mol. Gen. Genet. 246, 10-18, 1995
A:Title: Abscissic acid-dependent and -independent regulation of gene expression by proga
A:Reference number: S51478; MUID:95124290; PMID:7823904
A:Accession: S51479
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA
A:Residues: 1-104 <COS>
A:Cross-references: UNIPROT:Q39084; UNIPARC:UPI000000BF21; EMBL:X78585; NID:g469111; P
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
C:Genetics:
A:Gene: Di21
C:Superfamily: late embryogenesis-abundant protein lea5

Query Match 88.9%; Score 16; DB 2; Length 104;
Best Local Similarity 20.0%; Pred. No. 5.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
DB 14 CSAAGSLSC 23

RESULT 15

A71249
hypothetical protein PH0248 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: A71249
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sek
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguc
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: A71249
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-105 <KAW>
A:Cross-references: UNIPROT:O57986; UNIPARC:UPI0000062D66; GB:AP000001; NID:g3236128;
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBan
C:Genetics:
A:Gene: PH0248

Query Match 88.9%; Score 16; DB 2; Length 105;
Best Local Similarity 20.0%; Pred. No. 5.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
DB 35 CFTASASLAC 44

Search completed: May 2, 2006, 08:56:19
Job time : 19.1395 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 113.256 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	213	2	Q96KM3 HUMAN
2	18	100.0	263	2	Q586F4 9TRYP
3	18	100.0	269	2	Q7PRQ7 ANOGEA
4	18	100.0	281	2	Q5TX10 ANOGEA
5	18	100.0	313	1	YMS8 YEAST
6	18	100.0	357	2	Q6ZDR4 ORYSA
7	18	100.0	362	2	Q7QJL0 ANOGEA
8	18	100.0	480	2	Q9RV87 DEIRA
9	18	100.0	653	1	TMCC1 HUMAN
10	18	100.0	1005	2	Q5H3I7 XANOR
11	18	100.0	1061	2	Q4QCX7 LEIMA
12	17	94.4	52	2	Q8LPD6 HORVU
13	17	94.4	122	2	Q5DCN3 SCHJA
14	17	94.4	128	2	Q96LJ4 HUMAN
15	17	94.4	139	2	Q6ZKM7 ORYSA
16	17	94.4	155	2	Q6H482 ORYSA
17	17	94.4	160	2	Q657M0 ORYSA
18	17	94.4	160	2	Q4T4H1 TETNG
19	17	94.4	219	2	Q825E8 STRAW
20	17	94.4	220	2	Q66152 9VIRU
21	17	94.4	256	2	Q6VTS2 ORYSA
22	17	94.4	260	2	Q850Z3 ORYSA
23	17	94.4	304	2	Q5TVE4 ANOGEA
24	17	94.4	344	2	Q582B8 9TRYP
25	17	94.4	361	2	Q57Z20 9TRYP
26	17	94.4	364	2	Q4YM87 PLABE
27	17	94.4	368	2	Q7ORD3 GERHY
28	17	94.4	376	1	CBID AGRTS
29	17	94.4	388	2	Q7PYI3 ANOGEA
30	17	94.4	389	2	Q21081 CAEEL
31	17	94.4	411	2	Q67UZ3 ORYSA

32	17	94.4	437	2	Q4I4Q8 GIBZE
33	17	94.4	471	2	Q9VMG7 DROME
34	17	94.4	475	2	Q7X7A4 ORYSA
35	17	94.4	491	2	Q4P4C7 USTYMA
36	17	94.4	520	2	Q4XZV5 PLACH
37	17	94.4	556	2	Q803D5 BRARE
38	17	94.4	568	2	Q5GXM1 XANOR
39	17	94.4	626	2	Q4N2Y7 THEPA
40	17	94.4	630	2	Q69TY8 ORYSA
41	17	94.4	634	1	HSP71 LEIMA
42	17	94.4	635	2	Q4Q747 LEIMA
43	17	94.4	652	2	Q4Q740 LEIMA
44	17	94.4	660	2	Q4Q744 LEIMA
45	17	94.4	662	2	Q4Q745 LEIMA

ALIGNMENTS

RESULT 1
Q96KM3 HUMAN
ID Q56KM3 HUMAN PRELIMINARY; PRT; 213 AA.
AC Q96KM3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aberrant WW domain-containing oxidoreductase.
GN Name=WWOX;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
CX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE
RP MDLINE=21457335; PubMed=11572989; DOI=10.1073/pnas.191175898;
RA Paige A.J.W., Taylor K.J., Taylor C., Hillier S.G., Farrington S.,
RA Scott D., Porteous D.J., Smyth J.F., Gabra H., Watson J.E.V.;
RT "WWOX: a candidate tumor suppressor gene involved in multiple tumor
RT types";
RL Proc. Natl. Acad. Sci. U.S.A. 98:11417-11422(2001).
DR EMBL; AF325432; AAL05451.1; Genomic DNA.
DR EMBL; AF325423; AAL05451.1; JOINED; Genomic DNA.
DR EMBL; AF325424; AAL05451.1; JOINED; Genomic DNA.
DR EMBL; AF325426; AAL05451.1; JOINED; Genomic DNA.
DR EMBL; AF325433; AAL05451.1; JOINED; Genomic DNA.
DR EMBL; AF325425; AAL05451.1; JOINED; Genomic DNA.
DR HSSP; Q13526; IPIIN.
DR Ensembl; ENSG00000186153; Homo sapiens.
DR InterPro; IPR001202; WW_Rep5_WWP.
DR Pfam; PF00397; WW; 2.
DR SMART; SMO0456; WW; 2.
DR PROSITE; PS01159; WW DOMAIN 1; 2.
DR PROSITE; PS50020; WW DOMAIN 2; 2.
SQ SEQUENCE 213 AA; 23868 MW; A21054FF8214CCT7C CRC64;

Query Match 100.0%; Score 18; DB 2; Length 213;

Best Local Similarity 20.0%; Pred. No. 0.43;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 184 CTSTTAAAC 193

RESULT 2
Q586F4 9TRYP
ID Q586F4 9TRYP PRELIMINARY; PRT; 263 AA.
AC Q586F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.

GN ORFNames=Tb927.6.4820;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallow J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.;
RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Haas B., Blandin G., El-Sayed N.;
RN Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC008146; AAX80300.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 263 AA; 28873 MW; F61DF5AF910531AB CRC64;

Query Match 100.0%; Score 18; DB 2; Length 263;
Best Local Similarity 20.0%; Pred. No. 0.46; Mismatches 0; Indels 8; Gaps 0;
Matches 2; Conservative 0;

Qy 1 CXXXXXXXC 10
Db 95 CATTSSSSAC 104

RESULT 3
Q7PRQ7 ANOGA
ID Q7PRQ7 ANOGA PRELIMINARY; PRT; 269 AA.
AC Q7PRQ7;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ENSANGP0000001657 (Fragment).
GN ORFNames=ENSANGP0000001387;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008847; EAA06779.3; -; Genomic_DNA.
FT NON_TER 1 269
FT SEQUENCE 269 AA; 24228 MW; 25BPF71FD71F1F2 CRC64;
SQ SEQUENCE 269 AA; 24228 MW; 25BPF71FD71F1F2 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 269;
Best Local Similarity 20.0%; Pred. No. 0.47; Mismatches 0; Indels 8; Gaps 0;
Matches 2; Conservative 0;

Qy 1 CXXXXXXXC 10
Db 149 CTSSSSTTSC 158

RESULT 4
QSTX10 ANOGA
ID QSTX10 ANOGA PRELIMINARY; PRT; 281 AA.
AC QSTX10;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE ENSANGP00000027669 (Fragment).
GN ORFNames=ENSANGP00000007023;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008807; EAL41760.1; -; Genomic_DNA.
FT NON_TER 1 281
FT SEQUENCE 281 AA; 25341 MW; 0462E1169PB8642B CRC64;
SQ SEQUENCE 281 AA; 25341 MW; 0462E1169PB8642B CRC64;

Query Match 100.0%; Score 18; DB 2; Length 281;
Best Local Similarity 20.0%; Pred. No. 0.48; Mismatches 0; Indels 8; Gaps 0;
Matches 2; Conservative 0;

Qy 1 CXXXXXXXC 10
Db 107 CTAASSTAC 116

RESULT 5
YM58 YEAST
ID YM58 YEAST STANDARD; PRT; 313 AA.
AC Q03695;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 35.0 kDa protein in PFK2-HPA1 intergenic region.
DE OrderedLocustNames=YM206W; ORFNames=YM8325.07;
GN Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97333268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrell B.G.;
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008847; EAA06779.3; -; Genomic_DNA.
FT NON_TER 1 269
FT SEQUENCE 269 AA; 24228 MW; 25BPF71FD71F1F2 CRC64;
SQ SEQUENCE 269 AA; 24228 MW; 25BPF71FD71F1F2 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 269;
Best Local Similarity 20.0%; Pred. No. 0.47; Mismatches 0; Indels 8; Gaps 0;
Matches 2; Conservative 0;

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL; Z48755; CAAB8648.1; -; Genomic_DNA.
CC DR PR; S59448; S59448.
CC DR GernOnline; 142881; -.
CC DR Ensembl; YMR206N; Saccharomyces cerevisiae.
CC DR SGD; S000004819; YMR206W.
CC KW Complete proteome; Hypothetical protein.
CC FT COMPBIAS 3 6 Poly-Ser.
CC FT COMPBIAS 146 149 Poly-Gln.
CC FT COMPBIAS 246 252 Poly-Ser.
CC SQ SEQUENCE 313 AA; 35018 MW; 9D92BFE982577F0 CRC64;

Query Match 100.0%; Score 18; DB 1; Length 313;
Best Local Similarity 20.0%; Pred. No. 0.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CXXXXXXXC 10
Db 245 CXXXXXXXC 254

RESULT 6
Q6ZDR4 ORYSA
ID Q6ZDR4 ORYSA PRELIMINARY; PRT; 357 AA.
AC Q6ZDR4;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Putative transcription factor Myb protein.
GN Name=P0481F05.20;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;

RN NUCLEOTIDE SEQUENCE.
RP Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
RT clone: P0481F05.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AP004376; BAD09322.1; -; Genomic_DNA.
DR HSP; Q03237; 1A57.
DR Granene; Q6ZDR4; -.

DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00090; MYB_3; 2.
KW Nuclear protein; Repeat.

SQ SEQUENCE 357 AA; 36754 MW; 3F4F56860D3B4E22 CRC64;
Query Match 100.0%; Score 18; DB 2; Length 357;
Best Local Similarity 20.0%; Pred. No. 0.52;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CXXXXXXXC 10
Db 322 CSATASASSC 331

RESULT 7
Q7QJL0 ANOGA
ID Q7QJL0 ANOGA PRELIMINARY; PRT; 362 AA.

AC Q7QJL0;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE ENSANGP0000009383 (Fragment).
GN ORFNAMES=ENSANGS0000007023;
OS Anopheles gambiae str. PEST;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;

RN NUCLEOTIDE SEQUENCE.
RP The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PEST;
RC The Anopheles gambiae Sequence Committee;
RG The Anopheles gambiae re-annotation.
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RL [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PEST;
RC The Anopheles gambiae Sequence Committee;
RG The Anopheles gambiae re-annotation.
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAA01008007; EAA04378.2; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 362 AA; 32490 MW; 384376DDF431BEC0 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 362;
Best Local Similarity 20.0%; Pred. No. 0.52;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CXXXXXXXC 10
Db 187 CTAASSTAC 196

RESULT 8
Q9RV87 DEIRA
ID Q9RV87 DEIRA PRELIMINARY; PRT; 480 AA.
AC Q9RV87;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein DR1142.
GN OrderedLocName=DR1142;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIT 9279;
RC MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RX White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE001963; AAF10716.1; -; Genomic_DNA.
DR FIC; E75433; E75433.
DR TIGR; DR1142; -.

KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 480 AA; 49364 MW; 18B962ADA5CA24AE CRC64;
Query Match 100.0%; Score 18; DB 2; Length 480;
Best Local Similarity 20.0%; Pred. No. 0.58;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 464 CASAAATAAC 473

RESULT 9

TMCC1 HUMAN
ID TMCC1 HUMAN STANDARD; PRT; 653 AA.
AC O94876; O68506; O81X8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Transmembrane and coiled-coil domains protein 1.
GN Name=TMCC1; Synonyms=KIAA0779;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]

RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RC TISSUE=Skin;
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Nadan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 15-653.
RC TISSUE=Endometrial tumor;
RG The German CDNA Consortium;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

[3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 334-653.

RC TISSUE=Brain;

RX MEDLINE=99087487; PubMed=9872452;

RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,

RA Tanaka A., Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XI.

The complete sequences of 100 new cDNA clones from brain which code

for large proteins in vitro."

RL DNA Res. 5:277-286(1998)

CC -!- SIMILARITY: Belongs to the TEX28 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC ENBL; AB018322; BAA34499.1; -; mRNA.

DR ENBL; BC039859; AAH39859.1; -; mRNA.

DR ENBL; CR749206; CAH18064.2; -; mRNA.

DR Ensembl; ENSG00000172765; Homo sapiens.

DR HGNC; HGNC:29116; TMCC1.

KW Coiled coil; Transmembrane.
FT TRANSMEM 592 612 Potential.
FT TRANSMEM 625 645 Potential.
FT COILED 228 313 Potential.
FT COILED 458 576 Potential.
SQ SEQUENCE 653 AA; 72053 MW; 18B07D171B874205 CRC64;

Query Match 100.0%; Score 18; DB 1; Length 653;
Best Local Similarity 20.0%; Pred. No. 0.65;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 173 CAAAAAAAC 182

RESULT 10

Q5H317_XANOR PRELIMINARY; PRT; 1005 AA.
AC Q5H317;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Transcriptional regulator.
GN Name=acok; OrderedLocusNames=XOO1230;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
[1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=KACC10331 / XKO85;
RC PubMed=15673718; DOI=10.1093/nar/gki206;
RX Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
RA Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
RA Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
RA Go S.-J.;

"The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
the bacterial blight pathogen of rice."

RL Nucleic Acids Res. 33:577-586(2005).

DR EMBL; AF013598; AAW74484.1; -; Genomic DNA.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.

DR GO; GO:000166; F:nucleotide binding; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR000792; HTH_LuxR.

DR InterPro; IPR001440; TPR.

DR InterPro; IPR011717; TPR_4.

DR Pfam; PF00196; GexE; 1.

DR Pfam; PF00515; TPR_1; 2.

DR Pfam; PF07721; TPR_4; 1.

DR PRINTS; PR00038; HTH_LuxR.

DR ProDom; PD000307; HTH_LuxR; 1.

DR SMART; SM00382; AAA; 1.

DR SMART; SM00421; HTH_LuxR; 1.

DR SMART; SM00028; TPR; 3.

DR PROSITE; PS00622; HTH_LuxR_FAMILY; 1.

DR PROSITE; PS0293; TPR_REGION; 1.

KW Complete proteome.

SQ SEQUENCE 1005 AA; 110791 MW; 662961379FD37B61 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 1005;
Best Local Similarity 20.0%; Pred. No. 0.77;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 386 CASATTAAAC 395

RESULT 11

Q4QCK7 LEIMA
ID Q4QCK7 LEIMA PRELIMINARY; PRT; 1061 AA.
AC Q4QCK7
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DE Kinesin heavy chain, putative.
GN ORFNames=LmjF20.0640;
OS Leishmania major.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; C7005259; CAJ03791.1; -; Genomic DNA.
SQ SEQUENCE 1061 AA; 113930 MW; 2C69385D06371DCD CRC64;
Query Match 100.0%; Score 18; DB 2; Length 1061;
Best Local Similarity 20.0%; Pred. No. 0.79; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;
QY 1 CXXXXXXXC 10
DB 192 CAATATSC 201
RESULT 12
Q8LPD6 HORVU
ID Q8LPD6 HORVU PRELIMINARY; PRT; 52 AA.
AC Q8LPD6
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative glutathione-S-transferase (Fragment).
GN Name=bar2;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baldwin A.;
RT "The effect of thiocarbamate herbicides and the safener dichlorimid in
barley and wild oats."
RL Thesis (2001), Department of Cardiff School of Biosciences, Cardiff
university, Cardiff, United Kingdom.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Baldwin A., Harwood J.L., Machray G.C., Francis D., Rogers H.J.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ419772; CAD11963.1; -; mRNA.
DR HSP; P12653; IAXD
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR PRINTS; PR01590; HTHFIS.
KW Transferase.
FT NON TER 1
FT NON TER 52
SQ SEQUENCE 52 AA; 5750 MW; 7392EB72A3C70B9B CRC64;
Query Match 94.4%; Score 17; DB 2; Length 52;
Best Local Similarity 20.0%; Pred. No. 1.3;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CXXXXXXXC 10

DB 18 CTSASSTRSC 27
RESULT 13
Q5DCN3 SCHJA
ID Q5DCN3 SCHJA PRELIMINARY; PRT; 122 AA.
AC Q5DCN3
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes."
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY814691; AAW26423.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 122 AA; 13028 MW; 960E8615986958DE CRC64;
Query Match 94.4%; Score 17; DB 2; Length 122;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CXXXXXXXC 10
DB 76 CTESSSTSAC 85
RESULT 14
Q96LJ4 HUMAN
ID Q96LJ4 HUMAN PRELIMINARY; PRT; 128 AA.
AC Q96LJ4
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ25437.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058166; BAB71697.1; -; mRNA.
DR Ensembl; ENSG00000178093; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; Pkinase; 1
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Transferase.
SQ SEQUENCE 128 AA; 14116 MW; D30AC8C668621B0C CRC64;
Query Match 94.4%; Score 17; DB 2; Length 128;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CXXXXXXXC 10

Db 118 CTATSAKTC 127

RESULT 15

Q6ZKM7_ORYSA
 ID Q6ZKM7_ORYSA PRELIMINARY; PRT; 139 AA.
 AC Q6ZKM7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OJ1118_A06.7-1.
 GN Name=OJ1118_A06.7-1;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
 RT clone:OJ1118_A06";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003873; BAD08805.1; -; Genomic_DNA.
 DR Gramene; Q6ZKM7; -;
 KW Hypothetical protein.
 SQ SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;

Query Match 94.4%; Score 17; DB 2; Length 139;
 Best Local Similarity 20.0%; Pred. No. 1.9;
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXC 10
 Db 77 CAAITSSSSC 86

Search completed: May 2, 2006, 08:46:46
 Job time : 116.256 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 93.0233 Seconds
(without alignments)
44.917 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	33	4	US-10-697-399-10
2	18	100.0	37	4	US-10-380-927-7
3	18	100.0	328	4	US-10-286-115-800
4	18	100.0	339	5	US-10-287-436A-231
5	18	100.0	356	5	US-10-450-763-51398
6	18	100.0	405	5	US-10-287-436A-216
7	18	100.0	429	4	US-10-424-955A-28
8	18	100.0	447	5	US-10-287-436A-206
9	18	100.0	465	5	US-10-287-436A-257
10	18	100.0	545	5	US-10-287-436A-271
11	18	100.0	598	4	US-10-437-963-162631
12	18	100.0	630	3	US-09-791-279-86
13	18	100.0	647	4	US-10-184-644-539
14	18	100.0	647	4	US-10-184-634-539
15	18	100.0	653	3	US-09-374-046A-20
16	18	100.0	653	4	US-10-102-524-1851
17	18	100.0	653	4	US-10-331-496A-81
18	18	100.0	653	4	US-10-616-263-20
19	18	100.0	693	4	US-10-123-155-499
20	18	100.0	693	4	US-10-146-731-499
21	18	100.0	693	4	US-10-140-472-499
22	18	100.0	693	4	US-10-141-761-499
23	18	100.0	693	4	US-10-142-885-499
24	18	100.0	693	4	US-10-158-790-499
25	18	100.0	693	4	US-10-137-871-499
26	18	100.0	693	4	US-10-140-923-499
27	18	100.0	693	4	US-10-141-756-499

28	18	100.0	693	4	US-10-141-759-499	Sequence 499, App
29	18	100.0	693	4	US-10-140-805-499	Sequence 499, App
30	18	100.0	693	4	US-10-140-864-499	Sequence 499, App
31	18	100.0	733	4	US-10-437-963-129702	Sequence 129702,
32	18	100.0	735	4	US-10-184-644-167	Sequence 167, App
33	18	100.0	735	4	US-10-184-634-167	Sequence 167, App
34	18	100.0	755	4	US-10-123-155-153	Sequence 153, App
35	18	100.0	755	4	US-10-146-731-153	Sequence 153, App
36	18	100.0	755	4	US-10-140-472-153	Sequence 153, App
37	18	100.0	755	4	US-10-141-761-153	Sequence 153, App
38	18	100.0	755	4	US-10-142-885-153	Sequence 153, App
39	18	100.0	755	4	US-10-158-790-153	Sequence 153, App
40	18	100.0	755	4	US-10-137-871-153	Sequence 153, App
41	18	100.0	755	4	US-10-140-923-153	Sequence 153, App
42	18	100.0	755	4	US-10-141-756-153	Sequence 153, App
43	18	100.0	755	4	US-10-141-759-153	Sequence 153, App
44	18	100.0	755	4	US-10-140-805-153	Sequence 153, App
45	18	100.0	755	4	US-10-140-864-153	Sequence 153, App

ALIGNMENTS

RESULT 1
US-10-697-399-10
; Sequence 10, Application US/10697399
; Publication No. US20040162413A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Vassero, Alain P.
; APPLICANT: Marquis, David P.
; APPLICANT: Smith, Eric P.
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-08122
; CURRENT APPLICATION NUMBER: US/10/697,399
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-697-399-10

Query Match	100.0%	Score 18;	DB 4;	Length 33;
Best Local Similarity	20.0%	Pred. No. 2.2;		
Matches	2;	Conservative	0;	Mismatches 8;
				Indels 0;
				Gaps 0;
Qy	1	CXXXXXXC 10		
Db	24	CTATTAAAC 33		
RESULT 2 -				
US-10-380-927-7				
; Sequence 7, Application US/10380927				
; Publication No. US20040110165A1				
; GENERAL INFORMATION:				
; APPLICANT: Larry W. Kwak				
; APPLICANT: Arya Biragyn				
; TITLE OF INVENTION: VIRAL CHEMOKINE-ANTIGEN FUSION PROTEINS				
; FILE REFERENCE: 14014.0381U2				
; CURRENT APPLICATION NUMBER: US/10/380,927				
; CURRENT FILING DATE: 2003-12-04				
; PRIOR APPLICATION NUMBER: PCT/US01/29075				
; PRIOR FILING DATE: 2001-09-17				
; PRIOR APPLICATION NUMBER: 60/233,067				
; NUMBER OF SEQ ID NOS: 38				
; SOFTWARE: FastSeq for Windows Version 4.0				

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; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence = Note
; OTHER INFORMATION: Synthetic Construct
US-10-380-927-7

Query Match      100.0%; Score 18; DB 4; Length 37;
Best Local Similarity 20.0%; Pred. No. 2.3;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      7 CTTTATTTC 16

RESULT 3
US-10-296-115-800
; Sequence 800, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 800
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(328)
; OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
US-10-296-115-800

Query Match      100.0%; Score 18; DB 4; Length 328;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      63 CAAAAAAAC 72

RESULT 4
US-10-287-436A-231
; Sequence 231, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-231
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Query Match      100.0%; Score 18; DB 5; Length 339;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      314 CTTTTTAAC 323

RESULT 5
US-10-450-763-51398
; Sequence 51398, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CI3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51398
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (116)..(136)
; OTHER INFORMATION: RIBOKINASE SIGNATURE domain identified by eMATRIX, accession
; OTHER INFORMATION: number PR00990B, p-value=8.425e-10, raw score of 12.32
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(356)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-51398

Query Match      100.0%; Score 18; DB 5; Length 356;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXC 10
DB      183 CAAAAAAASC 192

RESULT 6
US-10-287-436A-216
; Sequence 216, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-216

Query Match      100.0%; Score 18; DB 5; Length 405;
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Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 340 CAAATAATC 349

RESULT 7

US-10-424-955A-28
; Sequence 28, Application US/10424955A
; Publication No. US20040014658A1
; GENERAL INFORMATION:
; APPLICANT: PROCHON BIOTECH LTD.
; APPLICANT: Bogin, Oren
; APPLICANT: Yayon, Avner
; APPLICANT: Adar, Rivka
; TITLE OF INVENTION: ACTIVE VARIANTS OF FGF WITH IMPROVED SPECIFICITY
; FILE REFERENCE: 139380 IL
; CURRENT APPLICATION NUMBER: US/10/424,955A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 139380 IL
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-424-955A-28

Query Match 100.0%; Score 18; DB 4; Length 429;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 397 CATTTTTC 406

RESULT 8

US-10-287-436A-206
; Sequence 206, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-206

Query Match 100.0%; Score 18; DB 5; Length 447;
Best Local Similarity 20.0%; Pred. No. 3.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 226 CAATTAAC 235

RESULT 9

US-10-287-436A-257
; Sequence 257, Application US/10287436A

Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-257

Query Match 100.0%; Score 18; DB 5; Length 465;
Best Local Similarity 20.0%; Pred. No. 3.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 445 CTAAATAAC 454

RESULT 10

US-10-287-436A-271
; Sequence 271, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 271
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-271

Query Match 100.0%; Score 18; DB 5; Length 545;
Best Local Similarity 20.0%; Pred. No. 3.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 367 CTATTTTAC 376

RESULT 11

US-10-437-963-162631
; Sequence 162631, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162631
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61704C.1.pep
US-10-437-963-162631

Query Match 100.0%; Score 18; DB 4; Length 598;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 148 CTASSSSSC 157

RESULT 12

US-09-791-279-86
; Sequence 86, Application US/09791279
; Publication No. US20030050456A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis
; APPLICANT: Lind, Peter

; TITLE OF INVENTION: No. US20030050456A1el G Protein-Coupled Receptors

; FILE REFERENCE: 00048.US1
; CURRENT APPLICATION NUMBER: US/09/791,279
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,715
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,725
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,712
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,606
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,602
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,604
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,822
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,710
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,689
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,690
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,716
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-791-279-86

Query Match 100.0%; Score 18; DB 3; Length 630;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 128 CTTTTTAAC 137

RESULT 13

US-10-184-644-539
; Sequence 539, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 539
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-184-644-539

Query Match 100.0%; Score 18; DB 4; Length 647;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 288 CTTAAAAAAC 297

RESULT 14

US-10-184-634-539
; Sequence 539, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 539
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-184-634-539

Query Match 100.0%; Score 18; DB 4; Length 647;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 288 CTTAAAAAAC 297

Tue May 2 12:32:38 2006

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RESULT 15
US-09-374-046A-20
; Sequence 20, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (114)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (290)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (601)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (604)
; US-09-374-046A-20

Query Match 100.0%; Score 18; DB 3; Length 653;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXX 10
Db 173 CAAAAAAAC 182

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Search completed: May 2, 2006, 09:32:39
Job time : 94.0233 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17 ; Search time 14.186 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pepl.*
2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pepl.*
8: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pepl.*
10: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pepl.*
12: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	25	11	US-11-217-995-24
2	18	100.0	36	11	US-11-174-341-161
3	18	100.0	370	11	US-11-217-995-37
4	18	100.0	407	11	US-11-079-463-10130
5	18	100.0	1197	11	US-11-178-230-10
6	18	100.0	1886	9	US-10-515-868-8
7	18	100.0	1894	9	US-10-194-487-97
8	18	100.0	1894	9	US-10-195-883-97
9	18	100.0	1894	9	US-10-195-888-97
10	18	100.0	1894	9	US-10-195-889-97
11	18	100.0	1517	11	US-11-241-631-5
12	18	100.0	4440	9	US-10-194-487-525
13	18	100.0	4440	9	US-10-195-883-525
14	18	100.0	4440	9	US-10-195-888-525
15	18	100.0	4440	9	US-10-195-889-525
16	17	94.4	211	11	US-11-172-740-1547
17	17	94.4	228	9	US-10-980-388-17
18	17	94.4	273	11	US-11-070-080-19
19	17	94.4	296	11	US-11-182-343-31
20	17	94.4	339	11	US-11-096-568A-19359
21	17	94.4	354	9	US-10-478-345-2

22	17	94.4	381	11	US-11-096-568A-19358	Sequence 19358, A
23	17	94.4	382	11	US-11-217-995-38	Sequence 38, Appl
24	17	94.4	383	11	US-11-096-568A-19357	Sequence 19357, A
25	17	94.4	639	9	US-10-915-002-247	Sequence 247, App
26	17	94.4	1076	9	US-10-131-826A-219	Sequence 219, App
27	17	94.4	1076	9	US-10-973-115B-219	Sequence 219, App
28	17	94.4	1076	9	US-10-137-873A-219	Sequence 219, App
29	17	94.4	1076	9	US-10-152-370-219	Sequence 219, App
30	17	94.4	1076	11	US-11-290-153-219	Sequence 35, Appl
31	17	94.4	1141	11	US-11-217-995-35	Sequence 36, Appl
32	17	94.4	1141	11	US-11-217-995-36	Sequence 269, App
33	17	94.4	1300	9	US-10-194-487-269	Sequence 269, App
34	17	94.4	1300	9	US-10-195-883-269	Sequence 269, App
35	17	94.4	1300	9	US-10-195-888-269	Sequence 269, App
36	17	94.4	1300	9	US-10-195-889-269	Sequence 269, App
37	17	94.4	1356	9	US-10-894-592-3	Sequence 3, Appli
38	17	94.4	1503	11	US-11-145-405B-5	Sequence 5, Appli
39	17	94.4	1652	11	US-11-241-631-1	Sequence 1, Appli
40	17	94.4	1743	9	US-10-194-487-451	Sequence 451, App
41	17	94.4	1743	9	US-10-195-883-451	Sequence 451, App
42	17	94.4	1743	9	US-10-195-888-451	Sequence 451, App
43	17	94.4	1743	9	US-10-195-889-451	Sequence 451, App
44	17	94.4	2508	11	US-11-241-631-7	Sequence 7, Appli
45	17	94.4	2544	11	US-11-241-631-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-11-217-995-24
; Sequence 24, Application US/11217995
; Publication No. US20060073142A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Chan
; APPLICANT: Robert Shields
; APPLICANT: Lauren Wu
; TITLE OF INVENTION: ANTI-FC-GAMMA RIIB RECEPTOR ANTIBODY AND USES THEREFOR.
; FILE REFERENCE: P1935R1
; CURRENT APPLICATION NUMBER: US/11/217,995
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 60/606,851
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 24
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-217-995-24

Query Match 100.0%; Score 18; DB 11; Length 25;
Best Local Similarity 20.0%; Pred. No. 9e+05;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CXXXXXXXC 10
DB 1 CAATTATTTTC 10

RESULT 2

US-11-174-341-161
; Sequence 161, Application US/11174341
; Publication No. US20060031967A1
; GENERAL INFORMATION:
; APPLICANT: Slade, Ann
; APPLICANT: Madisen, Linda
; APPLICANT: Comai, Luca
; TITLE OF INVENTION: Compositions and Methods for Modulation of Plant Cell
; TITLE OF INVENTION: Division
; FILE REFERENCE: 6769*2
; CURRENT APPLICATION NUMBER: US/11/174,341

; CURRENT FILING DATE: 2005-07-01
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Plant
US-11-174-341-161

Query Match 100.0%; Score 18; DB 11; Length 36;
Best Local Similarity 20.0%; Pred. No. 9.9e-05;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 19 CATTATAATC 28

RESULT 3

US-11-217-995-37
; Sequence 37, Application US/11217995
; Publication No. US20060073142A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Chan
; APPLICANT: Robert Shields
; APPLICANT: Lauren Wu
; TITLE OF INVENTION: ANTI-FC-GAMMA RIIB RECEPTOR ANTIBODY AND USES THEREFOR
; FILE REFERENCE: P1935R1
; CURRENT APPLICATION NUMBER: US/11/217,995
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 60/606,851
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-217-995-37

Query Match 100.0%; Score 18; DB 11; Length 370;
Best Local Similarity 20.0%; Pred. No. 0.00018;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 293 CATTATTATC 302

RESULT 4

US-11-079-463-10130
; Sequence 10130, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 10130
; LENGTH: 407
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-10130

Query Match 100.0%; Score 18; DB 11; Length 407;

Best Local Similarity 20.0%; Pred. No. 0.00018;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 5 CASATTSSAC 14

RESULT 5

US-11-178-230-10
; Sequence 10, Application US/11178230
; Publication No. US20060084162A1
; GENERAL INFORMATION:
; APPLICANT: Qasba, Pradman
; APPLICANT: Ramakrishnan, Boopathy
; APPLICANT: National Institutes of Health
; TITLE OF INVENTION: Catalytic Domains of (1,4)-Galactosyltransferase I Having Alter
; TITLE OF INVENTION: and Acceptor Specificities, Domains That Promote In Vitro Prote
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 1662.001US1
; CURRENT APPLICATION NUMBER: US/11/178,230
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/US2004/000470
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: US 60/439,298
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/450,250
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-178-230-10

Query Match 100.0%; Score 18; DB 11; Length 1197;
Best Local Similarity 20.0%; Pred. No. 0.00024;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 948 CATTTTTAAAC 957

RESULT 6

US-10-515-868-8
; Sequence 8, Application US/10515868
; Publication No. US20050282729A1
; GENERAL INFORMATION:
; APPLICANT: Hamilton, David W
; APPLICANT: Roberts, Kenneth P
; APPLICANT: Ensrud, Kathy M
; TITLE OF INVENTION: CRISP POLYPEPTIDES AS CONTRACEPTIVES AND INHIBITORS OF SPERM
; TITLE OF INVENTION: CAPACITATION
; FILE REFERENCE: 110.01860101
; CURRENT APPLICATION NUMBER: US/10/515,868
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/383,628
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: PCT/US03/16669
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1886
; TYPE: PRT
; ORGANISM: HOMOSAPIEN
US-10-515-868-8

Query Match 100.0%; Score 18; DB 9; Length 1886;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
|
Db 1359 CTATATATAC 1368

RESULT 7

US-10-194-487-97
; Sequence 97, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C312

; CURRENT FILING DATE: 2002-07-12

; PRIOR APPLICATION NUMBER: 60/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 97

; LENGTH: 1894

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-194-487-97

Query Match 100.0%; Score 18; DB 9; Length 1894;

Best Local Similarity 20.0%; Pred. No. 0.00027;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
|
Db 1154 CAATTAAAC 1163

RESULT 8

US-10-195-883-97
; Sequence 97, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C323

; CURRENT FILING DATE: 2002-07-15

; Prior Application removed - See File Wrapper or PALM

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 97

; LENGTH: 1894

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-195-883-97

Query Match 100.0%; Score 18; DB 9; Length 1894;

Best Local Similarity 20.0%; Pred. No. 0.00027;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
|
Db 1154 CAATTAAAC 1163

RESULT 9

US-10-195-888-97

; Sequence 97, Application US/10195888

; Publication No. US20060073545A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C324

; CURRENT FILING DATE: 2002-07-15

; Prior Application removed - See File Wrapper or PALM

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 97

; LENGTH: 1894

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-195-888-97

Query Match 100.0%; Score 18; DB 9; Length 1894;

Best Local Similarity 20.0%; Pred. No. 0.00027;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
|
Db 1154 CAATTAAAC 1163

RESULT 10

US-10-195-889-97

; Sequence 97, Application US/10195889

; Publication No. US20060074227A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C329
CURRENT APPLICATION NUMBER: US/10/195,889
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 97
LENGTH: 1894
TYPE: PRT
ORGANISM: Homo Sapien
US-10-195-889-97

Query Match 100.0%; Score 18; DB 9; Length 1894;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1154 CAATTAAC 1163

RESULT 11

US-11-241-631-5
Sequence 5, Application US/11241631
Publication No. US20060020115A1
GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.0009U4
CURRENT APPLICATION NUMBER: US/11/241,631
CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: US/10/156,240
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107,727
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1917
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-11-241-631-5

Query Match 100.0%; Score 18; DB 11; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1049 CAATATATC 1058

RESULT 12

US-10-194-487-525
Sequence 525, Application US/10194487
Publication No. US20060074226A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C312
CURRENT APPLICATION NUMBER: US/10/194,487
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 525
LENGTH: 4440.
TYPE: PRT
ORGANISM: Homo Sapien
US-10-194-487-525

Query Match 100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 3745 CTAATAATATC 3754

RESULT 13

US-10-195-883-525
Sequence 525, Application US/10195883
Publication No. US20060073544A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C323
CURRENT APPLICATION NUMBER: US/10/195,883
CURRENT FILING DATE: 2002-07-15

us-10-046-922-33.rapbn

Tue May 2 12:32:38 2006

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; FILE REFERENCE: P3430R1C329
; CURRENT APPLICATION NUMBER: US/10/195,889
; CURRENT FILLING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-889-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAATAATATC 3754

Search completed: May 2, 2006, 09:33:44
Job time : 15.186 secs

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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-889-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAATAATATC 3754

```

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RESULT 14
US-10-195-888-525
; Sequence 525, Application US/10195888
; Publication No. US20060073545A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C324
; CURRENT APPLICATION NUMBER: US/10/195,888
; CURRENT FILLING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-888-525

```

```

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAATAATATC 3754

```

```

RESULT 15
US-10-195-889-525
; Sequence 525, Application US/10195889
; Publication No. US20060074227A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 112.791 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	5	Abp53932 VEGFR-3 b
2	54	75.0	10	5	Abp53931 VEGFR-3 b
3	50	69.4	10	5	Abp53968 VEGFR-3 b
4	47.5	66.0	304	7	Adc87481 Human GPC
5	47	65.3	25	7	Adc99638 Cancer-re
6	46	63.9	17	6	Aao26074 Fc region
7	46	63.9	17	8	Adj50741 Human ser
8	46	63.9	136	8	Adm87650 Human EST
9	45	62.5	20	5	Aau90545 Insulin/i
10	45	62.5	129	2	Aay59880 Human nor
11	45	62.5	828	6	Abu49938 Protein e
12	44.5	61.8	1024	5	Abb04861 LDL recep
13	44	61.1	112	9	Aea18628 Amino aci
14	44	61.1	119	9	Aea18657 Amino aci
15	44	61.1	119	9	Aea18667 Amino aci
16	44	61.1	119	9	Aea18683 Amino aci
17	44	61.1	119	9	Aea18679 Amino aci
18	44	61.1	119	9	Aea18675 Amino aci
19	44	61.1	119	9	Aea18661 Amino aci
20	44	61.1	119	9	Aea18665 Amino aci
21	44	61.1	119	9	Aea18671 Amino aci
22	44	61.1	119	9	Aea18687 Amino aci
23	44	61.1	119	9	Aea18689 Amino aci
24	44	61.1	119	9	Aea18659 Amino aci

25	44	61.1	119	9	AEA18681	Aea18681 Amino aci
26	44	61.1	119	9	AEA18685	Aea18685 Amino aci
27	44	61.1	119	9	AEA18669	Aea18669 Amino aci
28	44	61.1	119	9	AEA18677	Aea18677 Amino aci
29	44	61.1	119	9	AEA18691	Aea18691 Amino aci
30	44	61.1	119	9	AEA18697	Aea18697 Amino aci
31	44	61.1	119	9	AEA18673	Aea18673 Amino aci
32	44	61.1	119	9	AEA18693	Aea18693 Amino aci
33	44	61.1	119	9	AEA18699	Aea18699 Amino aci
34	44	61.1	119	9	AEA18695	Aea18695 Amino aci
35	44	61.1	119	9	AEA18663	Aea18663 Amino aci
36	44	61.1	149	8	ADP29850	Adp29850 Human sec
37	44	61.1	166	6	AAE31487	Aae31487 Human but
38	44	61.1	415	5	AAU91293	Aau91293 Human NOV
39	44	61.1	468	9	AEA18640	Aea18640 Amino aci
40	43	59.7	13	6	AAO26093	Aao26093 Fc region
41	43	59.7	13	8	ADJ50760	Adj50760 Human ser
42	43	59.7	291	8	ADS30280	Ads30280 Bacterial
43	43	59.7	454	5	ABP73979	Abp73979 Candida a
44	43	59.7	474	6	ABU30004	Abu30004 Protein e
45	43	59.7	492	7	ADC97318	Adc97318 E. faeciu

ALIGNMENTS

RESULT 1
ABP53932
ID ABP53932 standard; peptide; 10 AA.
XX AC ABP53932;
XX DT 09-JAN-2003 (first entry)
XX DE VEGFR-3 binding peptide SEQ ID NO:35.

XX KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
XX KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
XX KW cytotatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
XX KW vulnary; cell surface receptor; cancer; neovascularisation;
XX KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
XX KW diabetes; PDGF; platelet derived growth factor.
XX OS Homo sapiens.
XX OS Synthetic.

Result No. Query Match Length DB ID Description

1	72	100.0	10	5	Abp53932 VEGFR-3 b
2	54	75.0	10	5	Abp53931 VEGFR-3 b
3	50	69.4	10	5	Abp53968 VEGFR-3 b
4	47.5	66.0	304	7	Adc87481 Human GPC
5	47	65.3	25	7	Adc99638 Cancer-re
6	46	63.9	17	6	Aao26074 Fc region
7	46	63.9	17	8	Adj50741 Human ser
8	46	63.9	136	8	Adm87650 Human EST
9	45	62.5	20	5	Aau90545 Insulin/i
10	45	62.5	129	2	Aay59880 Human nor
11	45	62.5	828	6	Abu49938 Protein e
12	44.5	61.8	1024	5	Abb04861 LDL recep
13	44	61.1	112	9	Aea18628 Amino aci
14	44	61.1	119	9	Aea18657 Amino aci
15	44	61.1	119	9	Aea18667 Amino aci
16	44	61.1	119	9	Aea18683 Amino aci
17	44	61.1	119	9	Aea18679 Amino aci
18	44	61.1	119	9	Aea18675 Amino aci
19	44	61.1	119	9	Aea18661 Amino aci
20	44	61.1	119	9	Aea18665 Amino aci
21	44	61.1	119	9	Aea18671 Amino aci
22	44	61.1	119	9	Aea18687 Amino aci
23	44	61.1	119	9	Aea18689 Amino aci
24	44	61.1	119	9	Aea18659 Amino aci

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 13; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) has cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of

CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a specifically claimed VEGFR-3 binding peptide from the
 CC present invention
 XX
 XX Sequence 10 AA;
 SQ

Query Match 100.0%; Score 72; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
 |||||
 Db 1 CGYWLTIWGC 10

RESULT 2
 ABP53931
 ID ABP53931 standard; peptide; 10 AA.
 XX
 AC ABP53931;
 XX
 DT 09-JAN-2003 (first entry)
 XX
 DE VEGFR-3 binding peptide SEQ ID NO:34.
 XX
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
 KW vulnary; cell surface receptor; cancer; neovascularisation;
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
 KW diabetes; PDGF; platelet derived growth factor.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "any amino acid"
 FT Misc-difference 10
 FT Misc-difference 10 /note= "any amino acid"
 FT
 XX
 PN WO200257299-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 16-JAN-2002; 2002WO-IB0000099.
 XX
 PR 17-JAN-2001; 2001US-0262476P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 XX
 XX Alitalo K, Koivunen E, Kubo H;
 PI
 XX WPI; 2002-691521/74.
 DR
 XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
 PT such as cancer and diseases of neovascularization.
 XX
 PS Claim 12; Page 80; 149pp; English.
 XX
 CC The present invention describes an isolated peptide (I) that binds to and
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
 CC antidiabetic and vulnary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 CC diagnosing, evaluating and treating disorders mediated by the activity of

CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a specifically claimed VEGFR-3 binding peptide from the
 CC present invention
 XX
 XX Sequence 10 AA;
 SQ

Query Match 75.0%; Score 54; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
 |||||
 Db 2 GYWLTIWG 9

RESULT 3
 ABP53968
 ID ABP53968 standard; peptide; 10 AA.
 XX
 AC ABP53968;
 XX
 DT 09-JAN-2003 (first entry)
 XX
 DE VEGFR-3 binding peptide SEQ ID NO:73.
 XX
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
 KW vulnary; cell surface receptor; cancer; neovascularisation;
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
 KW diabetes; PDGF; platelet derived growth factor.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 5..7 /note= "X is any amino acid"
 FT Misc-difference 9 /note= "X is any amino acid"
 FT
 XX
 PN WO200257299-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 16-JAN-2002; 2002WO-IB0000099.
 XX
 PR 17-JAN-2001; 2001US-0262476P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 XX
 XX Alitalo K, Koivunen E, Kubo H;
 PI
 XX WPI; 2002-691521/74.
 DR
 XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
 PT such as cancer and diseases of neovascularization.
 XX
 PS Disclosure; Page 147; 149pp; English.
 XX
 CC The present invention describes an isolated peptide (I) that binds to and
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
 CC antidiabetic and vulnary activities, and can be used in gene therapy.
 CC Compositions and methods from the present invention are useful for
 CC diagnosing, evaluating and treating disorders mediated by the activity of

CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
 CC skin, head and neck, esophagus, bone, marrow or blood, and diseases of
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence
 CC represents a VEGFR-3 binding peptide, which is given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 10 AA;

Query Match 69.4%; Score 50; DB 5; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.8;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
 |||||
 Db 1 CGYWLTIWGC 10

RESULT 4
 ADC87481
 ID ADC87481 standard; protein; 304 AA.

XX AC ADC87481;
 XX DT 01-JAN-2004 (first entry)
 XX DE Human GPCR protein SEQ ID NO:1934.
 XX KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
 XX KW gene therapy.
 XX OS Homo sapiens.

XX PN EP1270724-A2.
 XX PD 02-JAN-2003.
 XX PF 18-JUN-2002; 2002EP-00013517.
 XX PR 18-JUN-2001; 2001JP-00246789.
 XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX DR WPI; 2003-315783/31.
 XX DR N-PSDB; ADC87480.
 XX PT New polynucleotide, useful for preparing a composition for treating a
 XX PT patient in need of increased or suppressed activity or expression of the
 XX PT guanosine triphosphate-binding protein coupled receptor.

XX PS Claim 2; SEQ ID NO 1934; 28pp; English.
 XX CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The protein
 CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.

XX SQ Sequence 304 AA;
 Query Match 66.0%; Score 47.5; DB 7; Length 304;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWLTIWGC 10
 |||||

Db 108 CGFW-AVWGC 116

RESULT 5

ADC99638
 ID ADC99638 standard; peptide; 25 AA.

XX AC ADC99638;
 XX DT 01-JAN-2004 (first entry)
 XX DE Cancer-related Tie-1-binder peptide - SEQ ID 476.
 XX KW cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;
 KW leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;
 KW VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;
 KW kinase insert domain protein receptor; EGFR; epidermal growth factor;
 KW FGFR1; fibroblast growth factor; Tie-1.

XX OS Unidentified.

XX PN WO2003035839-A2.

XX PD 01-MAY-2003.

XX PF 24-OCT-2002; 2002WO-US034021.

XX PR 24-OCT-2001; 2001US-0345471P.

XX PA (DGI-B-) DGI BIOTECHNOLOGIES INC.

XX PI Pillutla RC, Brissette R, Spruyt M, Dedova O, Blume A;
 PI Prendergast J, Goldstein N;

XX DR WPI; 2003-457332/43.

XX PT Selecting target and target binder pairs for preparing a composition for
 PT treating cancer by mixing in a reaction vessel phase expressing
 PT biological targets and phase expressing target binders.

XX PS Claim 26; SEQ ID NO 476; 172pp; English.

XX CC The invention relates to a novel method of selecting target and target
 CC binder pairs comprising mixing in a reaction vessel phase expressing
 CC biological targets and phase expressing target binders, each having
 CC distinguishable selection markers and selecting target and target binder
 CC pairs based on the selection markers. The molecules of the invention
 CC demonstrate cytostatic activity whilst the method may be useful for
 CC selecting target and target binder pairs for preparing a composition for
 CC treating cancer. Furthermore, the method may be utilised during gene
 CC therapy procedures. The current sequence is that of the cancer-related
 CC Tie1-binder peptide of the invention.

XX SQ Sequence 25 AA;

Query Match 65.3%; Score 47; DB 7; Length 25;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9
 |||||

Db 5 CGYWLTIWGC 13

RESULT 6

AAO26074
 ID AAO26074 standard; peptide; 17 AA.

XX AC AAO26074;

XX DT 03-APR-2003 (first entry)

XX DE Fc region binding peptide SEQ ID No 54.

XX Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;
KW antibody response; half-life; stability; circulatory system.
XX Unidentified.
OS WO200286070-A2.
XX
XX 31-OCT-2002.
XX
XX 18-APR-2002; 2002WO-US012492.
XX
XX 18-APR-2001; 2001US-0284534P.
XX (DYAX-) DYAX CORP.
XX
XX Rondon IJ, Wu Q, Ley AC, Stochl M, Ranschoff TC, Potter MD;
PI WPI; 2003-201220/19.
XX
XX New polypeptides, useful as binding molecules for detecting, isolating or
XX purifying immunoglobulin Fc-region polypeptides present in a solution, or
XX for regulating or preventing an antibody response.
XX
XX Claim 3; Page 76; 152pp; English.
XX
XX The invention relates to novel isolated polypeptides comprising a
CC sequence that binds an immunoglobulin Fc region. The polypeptides are
CC useful as binding molecules for detecting, isolating or purifying
CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole
CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are
CC also useful for regulating or preventing an antibody response, or for
CC increasing the half-life and over all stability of a therapeutic or
CC diagnostic compound that is administered to or enters the circulatory
CC system of an individual. This sequence represents an Fc region binding
CC peptide of the invention
XX
XX Sequence 17 AA;
XX
XX Query Match 63.9%; Score 46; DB 6; Length 17;
XX Best Local Similarity 66.7%; Pred. No. 15;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CGYWLTIWG 9
XX ||| |||
XX 4 CGFWPRWG 12
XX
XX
XX RESULT 7
XX ADJ50741
XX ID ADJ50741 standard; peptide; 17 AA.
XX
XX AC ADJ50741;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human serum albumin binding peptide, Seq ID-No 278.
XX
XX human serum albumin; HSA; serum; blood; tumour; human.
XX
XX Homo sapiens.
XX
XX WO2003106493-A1.
XX
XX 24-DEC-2003.
XX
XX 16-JUN-2003; 2003WO-US018896.
XX
XX 14-JUN-2002; 2002US-0388642P.
XX (DYAX-) DYAX CORP.
XX
XX Sato AK, Dawson BM;
PI

XX WPI; 2004-082161/08.
XX
XX Evaluating sample comprising soluble serum protein by forming complex
XX comprising serum protein and physically associated compounds using
XX peptide ligand that specifically binds with proteins, which is separated
XX and evaluated.
XX
XX Disclosure; SEQ ID NO 278; 191pp; English.
XX
XX The invention relates to a method of evaluating sample by providing a
XX soluble serum protein (I), one or more compounds physically associated
XX with (I), and a (I)-binding agent that comprises a peptide that
XX specifically binds to (I), allowing the (I)-binding agent to bind to (I)
XX to form a complex including one or more compounds physically associated
XX with (I), separating the complex from one or more components of the
XX sample, and evaluating one or more of the physically associated
XX compounds. The sample comprises blood or serum, or is obtained from a
XX biopsy. The sample may also be obtained from a tumour or a region within
XX 5 mm of a tumour. The method is useful for detecting modulators that
XX modulate interaction of serum protein-binding compound and serum protein
XX and for identifying binding ligands for serum protein. The present
XX sequence represents a serum albumin-binding peptide identified using the
XX method of the invention.
XX
XX Sequence 17 AA;
XX
XX Query Match 63.9%; Score 46; DB 8; Length 17;
XX Best Local Similarity 66.7%; Pred. No. 15;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CGYWLTIWG 9
XX ||| |||
XX 4 CGFWPRWG 12
XX
XX
XX RESULT 8
XX ADM87650
XX ID ADM87650 standard; protein; 136 AA.
XX
XX AC ADM87650;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human EST derived amino acid sequence SEQ ID NO:743.
XX
XX respiratory; cytostatic; antiarthritic; antiinflammatory;
XX gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
XX antirheumatic; gene therapy; molecular weight marker; chromosome marker;
XX chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
XX inflammatory condition; arthritis; inflammatory bowel disease;
XX Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
XX graft versus host disease; human; expressed sequence tag; EST.
XX
XX Homo sapiens.
XX
XX WO2004009834-A2.
XX
XX 29-JAN-2004.
XX
XX 19-JUL-2002; 2002WO-US022858.
XX
XX 21-JUL-2001; 2001US-0306971P.
XX 28-MAR-2002; 2002US-00112944.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
XX Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
XX WPI; 2004-143291/14.
XX N-PSDB; ADM87432.
XX

PT New isolated polynucleotides and polypeptides, useful for treating, e.g.
 PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
 PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 PT versus host disease.

XX Example 2; SEQ ID NO 743; 591pp; English.

XX The present invention describes an isolated polynucleotide (I): (a)
 CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b).
 CC which encodes a polypeptide with biological activity, where the
 CC polynucleotide hybridizes to (I) under stringent hybridisation conditions
 CC or has greater than 98% sequence identity with (I). (I) has respiratory,
 CC cytosolic, antiarthritic, antiinflammatory, gastrointestinal,
 CC antibacterial, immunosuppressive, antidiabetic and antirheumatic
 CC activities, and can be used in gene therapy. (I) can be used for
 CC generating polynucleotides encoding chimeric or fusion proteins and
 CC heterologous protein sequences. The polynucleotides can be used to
 CC express recombinant protein for analysis, characterisation or therapeutic
 CC use; as markers for tissues in which the corresponding protein is
 CC preferentially expressed; as molecular weight markers on gels; as
 CC chromosome markers or tags to identify chromosomes or to map related gene
 CC positions; to compare with endogenous DNA sequences in patients to
 CC identify potential genetic disorders; as probes to hybridise and discover
 CC genes, related DNA sequences; as a source of information to derive PCR
 CC primers for genetic fingerprinting; as a probe to subtract-out known
 CC sequences in the process of discovering other novel polynucleotides; for
 CC selecting and making oligomers for attachment to a gene chip or other
 CC support, including for examination of expression patterns; to raise anti-
 CC protein antibodies using DNA immunisation techniques; and as an antigen
 CC to raise anti-DNA antibodies or elicit another immune response. The
 CC polynucleotides and polypeptides can also be used as nutritional sources
 CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
 CC source, as a nitrogen source or as a source of carbohydrates. The
 CC polynucleotides and polypeptides can also be used to treat cancer. The
 CC compositions are useful for promoting better or faster closure of non-
 CC healing wounds, for the generation and regeneration of tissues, for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, and conditions resulting from
 CC systemic cytokine damage. The compositions can also be used to treat
 CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
 CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
 CC or graft versus host disease. The present sequence represents an
 CC expressed sequence tag (EST) derived amino acid sequence from the present
 CC invention. N.B. The sequences for this patent were obtained from the
 CC USPTO web site from an equivalent US patent US20040048249A1.

XX Sequence 136 AA;

Query Match 63.9%; Score 46; DB 8; Length 136;
 Best Local Similarity 60.0%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
 ||| :|||
 Db 93 CGRWDLWGC 102

RESULT 9
 AAU90545
 ID AAU90545 standard; peptide; 20 AA.

XX AAU90545;

XX 18-JUN-2002 (first entry)

DE Insulin/insulin-like growth factor receptor-binding peptide #2501.

XX Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.

XX Synthetic.

XX WO200172771-A2.

XX 04-OCT-2001.

XX 29-MAR-2000; 2000WO-US008528.

XX 29-MAR-2000; 2000WO-US008528.

XX (DGIB-) DGI BIOTECHNOLOGIES LLC.

PA (NOVO) NOVO NORDISK AS.

XX Beasley J, Blume AJ, Schaeffer L, Pillutia R, Brandt J;

PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;

PI Hansen PH, Raveřa M, Hsiao K,

XX WPI; 2002-025774/03.

XX Modulating insulin activity in mammalian cells, for treating e.g.
 PT diabetes and tumors, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors.

XX Disclosure; Fig 8-3; 390pp; English.

XX The invention relates to a method of modulating insulin activity in
 CC mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
 CC IGF-1 receptor-binding peptides and related amino acid sequences of the
 CC invention

XX Sequence 20 AA;

Query Match 62.5%; Score 45; DB 5; Length 20;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
 ||| :|||
 Db 8 CGAWPTYWNC 17

RESULT 10
 AAU59880
 ID AAU59880 standard; protein; 129 AA.

XX AAU59880;

XX 19-JAN-2000 (first entry)

XX Human normal uterus tissue derived protein 43.

XX Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;
 KW EST; expressed sequence tag.

XX Homo sapiens.

XX DE19817946-A1.

XX 21-OCT-1999.

XX 17-APR-1998; 98DE-01017946.

XX 17-APR-1998; 98DE-01017946.

(META-) METAGEN GES GENOMFORSCHUNG MBH.

PA Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
XX MPI; 1999-591956/51.
XX N-PSDB; AAZ41339.

PT New nucleic acid sequences expressed in normal uterine tissues, and
XX derived polypeptides, for treatment of uterine cancer and identification
XX of therapeutic agents.

PS Claim 23; Page 138; 154pp; German.

CC This invention describes novel cDNA sequences (A) highly expressed in
XX normal uterine tissue which can have anticancer and cytostatic activity
XX and can be used for gene therapy. (A) are used (i) for recombinant
XX expression of polypeptides (B) and (ii) to isolate complete genes. (B)
XX are used (i) to identify agents suitable for treatment of uterine cancer;
XX (ii) directly for treating this form of cancer (including expression from
XX gene therapy vectors) and (iii) for generation of specific antibodies.
XX (A) are identified by assembling ESTs (expressed sequence tags) from a
XX particular tissue type before comparison of expression patterns. This
XX allows a significantly longer fragment of the gene to be revealed, so
XX from different libraries may represent different parts of the same
XX unknown gene, distorting the estimated frequency of occurrence in a
XX the human uterine tissue. AAV59838-Y59892 represent protein fragments encoded by
XX Z41385

XX Sequence 129 AA;
XX
XX Query Match 62.5%; Score 45; DB 2; Length 129;
XX Best Local Similarity 62.5%; Pred. No. 1.2e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGVWLTW 8
DB 32 CSHWLTW 39

RESULT 11
ABU49938
ID ABU49938 standard; protein; 828 AA.
XX
XX AC ABU49938;
XX
XX DT 19-JUN-2003 (first entry)
XX
XX DE Protein encoded by Prokaryotic essential gene #35465.
XX
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX OS Yersinia pestis.
XX
XX PN WO200277183-A2.
XX
XX PD 03-OCT-2002.
XX
XX PF 21-MAR-2002; 2002WO-US009107.
XX
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 08-MAR-2002; 2002US-0362659P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX PI Wang L, Zamudio C, Malone G, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX MPI; 2003-029926/02.

N-PSDB; ACA53808.

New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 77862; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway,
or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

Sequence 828 AA;
Query Match 62.5%; Score 45; DB 6; Length 828;
Best Local Similarity 58.3%; Pred. No. 5.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGVWLTW--WGC 10
DB 372 CGLWLELLSWGC 383

RESULT 12
ABB04861
ID ABB04861 standard; protein; 1024 AA.
XX
XX AC ABB04861;
XX
XX DT 13-MAR-2002 (first entry)
XX
XX DE LDL receptor binding protein Na channel brain 3 SEQ ID NO:84.
XX
XX KW Low density lipoprotein receptor binding protein; signal transduction;
XX LDL receptor binding protein; LDL receptor signalling pathway.
XX
XX OS Synthetic.
XX
XX PN WO200184159-A2.
XX
XX PD 08-NOV-2001.
XX
XX PF 24-APR-2001; 2001WO-US013214.
XX
XX PR 01-MAY-2000; 2000US-00562737.

XX (TEXA) UNIV TEXAS SYSTEM.
PA Herz J, Gotthardt M;
XX WPI; 2002-082855/11.
XX
XX Detecting stress that alters interaction of LDL receptor binding
PT polypeptide with LDL receptor interaction domain, comprises detecting
PT difference in stress-biased and unbiased interaction of peptide and
PT domain in a system.
XX
XX Disclosure; Page 148-150; 200pp; English.
XX
XX The present invention describes a method for detecting a stress that
CC alters a functional interaction of a low density lipoprotein (LDL)
CC receptor binding protein (I) with an LDL receptor interaction domain
CC (II). The method involves introducing a predetermined stress into a
CC system which provides a stress-biased physical interaction of (I) with
CC (II), where in the absence of the stress, the system provides an unbiased
CC interaction of (I) and (II), and detecting the stress-biased interaction
CC of (I) and (II), where a difference between BI and UI indicates that the
CC stress alters the interaction of (I) and (II). (I) is selected from
CC SEMCAP-1, JIP-1, PSD-95, JIP-2, Talin, OMP25, CAPON, PIP4, 5 Kinase, Na
CC channel brain 3, Mint1, ICAP-1 and APC subunit 10. The method is useful
CC for detecting a stress that alters functional interaction of LDL receptor
CC binding polypeptide with LDL receptor interaction domain. The method is
CC useful for detecting and modulating signal transduction through LDL
CC receptors. ABB04778 to ABB04909 represent LDL receptor binding proteins
CC which are used in the exemplification of the present invention
XX
XX Sequence 1024 AA;
XX
Query Match 61.8%; Score 44.5; DB 5; Length 1024;
Best Local Similarity 54.5%; Pred. NO. 7.8e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 CGYWL-TIWGC 10
DB 892 CGHWIETWDC 902
||:|:|:|
||:|:|:|
RESULT 13
AEA18628
ID AEA18628 standard; peptide; 112 AA.
XX
XX AEA18628;
XX
XX 28-JUL-2005 (first entry)
XX
XX Amino acid sequence of variable heavy chain region of murine B-Ly1.
XX
XX antigen binding molecule; Fc receptor; B-cell marker; CD20;
XX antibody engineering; B-cell depletion; B cell lymphoma; cytostatic;
XX hematological disease; immune disorder; neoplasm; heavy chain;
XX B-Ly1 antibody.
XX
XX Mus sp.
XX OS
XX WO2005044859-A2.
XX PN
XX 19-MAY-2005.
XX PD
XX 05-NOV-2004; 2004WO-IB003896.
XX PF
XX 05-NOV-2003; 2003US-0517096P.
XX PR
XX (GLYC-) GLYCART BIOTECHNOLOGY AG.
XX (UMAN/) UMANA P.
XX (BRUE/) BRUENKER P.
XX (FERR/) FERRARA C.
XX (SUTE/) SUTER T.
XX (PUEN/) PUENTENER U.
XX
XX Umana P, Bruenker P, Ferrara C, Suter T, Puentener U, Moessner E;
XX WPI; 2005-347056/35.
XX N-PSDB; AEA18656.

PA (MOES/) MOESSNER E.
XX Umana P, Bruenker P, Ferrara C, Suter T, Puentener U, Moessner E;
XX WPI; 2005-347056/35.
XX N-PSDB; AEA18629.
XX
XX New polynucleotides and encoded antigen binding molecules with increased
PT Fc receptor binding affinity and effector function, useful for
PT diagnosing, preventing or treating B-cell proliferative disorders,
PT including B cell lymphoma.
XX
XX Claim 9; SEQ ID NO 1; 187pp; English.
XX
XX The specification describes antigen binding molecules with increased Fc
CC receptor binding affinity and effector function. These antigen binding
CC molecules may have modified glycosylation, and are especially specific
CC for human B-cell marker CD20. The invention is useful for diagnosing,
CC preventing or treating disorders or diseases treatable by B-cell
CC depletion, such as B cell lymphoma. The present sequence represents the
CC variable heavy chain region of the murine antibody B-Ly1, and antibody
CC which binds CD20. The sequence is used to produce antigen binding
CC molecules of the invention.
XX
XX Sequence 112 AA;
XX
Query Match 61.1%; Score 44; DB 9; Length 112;
Best Local Similarity 75.0%; Pred. NO. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTIWG 9
DB 96 GYWLVIWG 103
|||||
|||||
RESULT 14
AEA18657
ID AEA18657 standard; protein; 119 AA.
XX
XX AEA18657;
XX
XX 28-JUL-2005 (first entry)
XX
XX Amino acid sequence of CD20 antigen binding molecule #1.
XX
XX antigen binding molecule; Fc receptor; B-cell marker; CD20;
XX antibody engineering; B-cell depletion; B cell lymphoma; cytostatic;
XX hematological disease; immune disorder; neoplasm.
XX
XX Mus sp.
XX OS
XX Homo sapiens.
XX OS
XX Chimeric.
XX
XX WO2005044859-A2.
XX PN
XX 19-MAY-2005.
XX PD
XX 05-NOV-2004; 2004WO-IB003896.
XX PF
XX 05-NOV-2003; 2003US-0517096P.
XX PR
XX (GLYC-) GLYCART BIOTECHNOLOGY AG.
XX (UMAN/) UMANA P.
XX (BRUE/) BRUENKER P.
XX (FERR/) FERRARA C.
XX (SUTE/) SUTER T.
XX (PUEN/) PUENTENER U.
XX (MOES/) MOESSNER E.
XX
XX Umana P, Bruenker P, Ferrara C, Suter T, Puentener U, Moessner E;
XX WPI; 2005-347056/35.
XX N-PSDB; AEA18656.

XX New polynucleotides and encoded antigen binding molecules with increased
PT Fc receptor binding affinity and effector function. These antigen binding
PT molecules may have modified glycosylation, and are especially specific
PT for human B-cell marker CD20. The invention is useful for diagnosing,
PT preventing or treating disorders or diseases treatable by B-cell
XX depletion, such as B cell lymphoma.
PS Claim 128; SEQ ID NO 30; 187pp; English.
XX
XX The specification describes antigen binding molecules with increased Fc
CC receptor binding affinity and effector function. These antigen binding
CC molecules may have modified glycosylation, and are especially specific
CC for human B-cell marker CD20. The invention is useful for diagnosing,
CC preventing or treating disorders or diseases treatable by B-cell
CC depletion, such as B cell lymphoma. The present sequence represents an
CC antigen binding molecule of the invention.
XX
SQ Sequence 119 AA;
Query Match 61.1%; Score 44; DB 9; Length 119;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTVWG 9
DB 103 GYWLTVWG 110
Search completed: May 2, 2006, 08:54:58
Job time : 114.791 secs

CC The specification describes antigen binding molecules with increased Fc
CC receptor binding affinity and effector function. These antigen binding
CC molecules may have modified glycosylation, and are especially specific
CC for human B-cell marker CD20. The invention is useful for diagnosing,
CC preventing or treating disorders or diseases treatable by B-cell
CC depletion, such as B cell lymphoma. The present sequence represents an
CC antigen binding molecule of the invention.
XX
SQ Sequence 119 AA;
Query Match 61.1%; Score 44; DB 9; Length 119;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTVWG 9
DB 103 GYWLTVWG 110
Search completed: May 2, 2006, 08:54:58
Job time : 114.791 secs

XX New polynucleotides and encoded antigen binding molecules with increased
PT Fc receptor binding affinity and effector function, useful for
PT diagnosing, preventing or treating B-cell proliferative disorders,
PT including B cell lymphoma.
XX
PS Claim 128; SEQ ID NO 30; 187pp; English.
XX
XX The specification describes antigen binding molecules with increased Fc
CC receptor binding affinity and effector function. These antigen binding
CC molecules may have modified glycosylation, and are especially specific
CC for human B-cell marker CD20. The invention is useful for diagnosing,
CC preventing or treating disorders or diseases treatable by B-cell
CC depletion, such as B cell lymphoma. The present sequence represents an
CC antigen binding molecule of the invention.
XX
SQ Sequence 119 AA;
Query Match 61.1%; Score 44; DB 9; Length 119;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTVWG 9
DB 103 GYWLTVWG 110

RESULT 15
AEA18667
ID AEA18667 standard; protein; 119 AA.
XX
AC AEA18667;
XX
DT 28-JUL-2005 (first entry)
XX
DE Amino acid sequence of CD20 antigen binding molecule #6.
XX
KW antigen binding molecule; Fc receptor; B-cell marker; CD20;
KW antibody engineering; B-cell depletion; B cell lymphoma; cytostatic;
KW hematological disease; immune disorder; neoplasm.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO2005044859-A2.
XX
PD 19-MAY-2005.
XX
PF 05-NOV-2004; 2004WO-1B003896.
XX
PR 05-NOV-2003; 2003US-0517096P.
XX
XX (GLYC-) GLYCART BIOTECHNOLOGY AG.
PA (UMAN/) UMANA P.
PA (BRUE/) BRUENKER P.
PA (FERR/) FERRARA C.
PA (SUTE/) SUTER T.
PA (PUEN/) PUENTENER U.
PA (MOES/) MOESSNER E.
XX
XX Umana P, Bruenker P, Ferrara C, Suter T, Puentener U, Moessner E;
XX WPI: 2005-347056/35.
XX N-PSDB; AEA18666.
XX
XX New polynucleotides and encoded antigen binding molecules with increased
PT Fc receptor binding affinity and effector function, useful for
PT diagnosing, preventing or treating B-cell proliferative disorders,
PT including B cell lymphoma.
XX
PS Claim 128; SEQ ID NO 40; 187pp; English.
XX

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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 18.1395 seconds

(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-35

Perfect score: 72

Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	63.9	218	2 S76385	hypothetical prote
2	45	62.5	828	2 AD0412	ATP-dependent heli
3	43.5	60.4	1993	2 T30902	sodium channel sca
4	42.5	59.0	1765	2 T42388	sodium channel alp
5	42	58.3	72	2 S30980	gene 35 protein -
6	42	58.3	441	2 C95307	probable transport
7	42	58.3	1502	2 T42216	multidrug resist
8	41.5	57.6	620	2 F70439	oxalacetate decar
9	41	56.9	307	2 T48166	hypothetical prote
10	41	56.9	391	2 PC4117	replication protei
11	41	56.9	419	2 E90446	permease [importe
12	41	56.9	739	2 T29407	hypothetical prote
13	40.5	56.2	200	2 I48108	sodium channel alp
14	40.5	56.2	1681	2 A45138	sodium channel mNa
15	40.5	56.2	1682	2 A45380	sodium channel pro
16	40.5	56.2	1820	1 CHEE	sodium channel alp
17	40.5	56.2	1835	2 I54323	sodium channel alp
18	40.5	56.2	1836	2 I64893	sodium channel alp
19	40.5	56.2	1836	2 J50648	sodium channel alp
20	40.5	56.2	1836	2 I51964	sodium channel alp
21	40.5	56.2	1840	1 CHRTM1	sodium channel pro
22	40.5	56.2	1951	2 S00320	sodium channel pro
23	40.5	56.2	1976	2 I56555	sodium channel alp
24	40.5	56.2	1977	2 S54771	sodium channel pro
25	40.5	56.2	1983	2 A60054	sodium channel alp
26	40.5	56.2	2005	2 A46269	sodium channel pro
27	40.5	56.2	2005	2 B25019	sodium channel pro
28	40.5	56.2	2009	2 A25019	sodium channel pro
29	40.5	56.2	2016	2 A38195	sodium channel pro

30	40.5	56.2	2019	2 A33996	sodium channel pro
31	40.5	56.2	2049	2 T43161	sodium channel pro
32	40	55.6	142	2 C34903	Ig heavy chain pre
33	40	55.6	339	2 F97190	phenylalanyl-tRNA
34	40	55.6	359	2 F95406	probable ABC trans
35	40	55.6	425	2 B71038	probable Na+/H+-ex
36	40	55.6	508	2 C95282	probable ABC trans
37	40	55.6	2344	2 S64740	genome polyprotein
38	39.5	54.9	298	2 AH0289	probable aldo/keto
39	39.5	54.9	345	1 JH0185	D-amino-acid oxida
40	39.5	54.9	347	1 OXPGDA	D-amino-acid oxida
41	39.5	54.9	347	1 S01340	D-amino-acid oxida
42	39.5	54.9	347	1 JX0132	hypothetical prote
43	39	54.2	376	2 AF1978	neurexin III beta
44	39	54.2	392	2 A53580	neurexin III beta
45	39	54.2	426	2 B53580	neurexin III beta

ALIGNMENTS

RESULT 1

S76385
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76385
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasu
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocyst
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76385
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <XAN>
A;Cross-references: UNIPROT:Q55705; UNIPARC:UPI00001394C5; EMBL:D64000; GB:AB001339; N
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: probable alkaline phosphatase yngC

Query Match 63.9%; Score 46; DB 2; Length 218;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGYWLTIWGC 9
Db 73 CGYWVGWGW 81
RESULT 2
AD0412
ATP-dependent helicase [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0412
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0412
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-828 <KUR>
A;Cross-references: UNIPROT:Q82BL4; UNIPARC:UPI00000CDA15; GB:AL590842; PIDN:CAC92624.
C;Genetics:
A;Gene: hrpB
C;Superfamily: ATP-dependent RNA helicase, HrpB type
Query Match 62.5%; Score 45; DB 2; Length 828;

Best Local Similarity 58.3%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10
||| : |||
Db 372 CGLWLELLSWGC 383

RESULT 3
T30902
sodium channel SCAP1 alpha chain - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30902
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol 16, 347-356, 1997
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
A;Accession: T30902
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1993 <DYE>
A;Cross-references: UNIPROT:P90670; UNIPARC:UPI000007A0B4; EMBL:U66915; NID:g1842248; PI
C;Superfamily: sodium channel protein

Query Match 60.4%; Score 43.5; DB 2; Length 1993;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
||| : |||
Db 942 CGEWIESMWGC 952

RESULT 4
T42388
sodium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42388
R;Dib-Hajj, S.D.; Tyrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
A;Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in peripheral
A;Reference number: 722149; MUID:98338024; PMID:9671787
A;Accession: T42388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1765 <DIB>
A;Cross-references: UNIPROT:O88457; UNIPARC:UPI00000E9ABD; EMBL:AF059030; NID:g3372614;
A;Experimental source: strain Sprague-Dawley; dorsal root ganglia
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trigem
C;Superfamily: sodium channel protein

Query Match 59.0%; Score 42.5; DB 2; Length 1765;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
||| : |||
Db 754 CGEWIENWGC 764

RESULT 5
S30980
gene 35 protein - Mycobacterium phage L5
C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S30980
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans
A;Reference number: S30949; MUID:93211283; PMID:8459767
A;Accession: S30980

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-72 <DON>
A;Cross-references: UNIPROT:O05245; UNIPARC:UPI0000138557; EMBL:Z18946; NID:g15859; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C;Genetics:
A;Gene: 35

Query Match 58.3%; Score 42; DB 2; Length 72;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8
||| : |||
Db 50 CGMWLPFW 57

RESULT 6
C95307
probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) m
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 05-Oct-2004
C;Accession: C95307
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bo
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95307
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 <KUR>
A;Cross-references: UNIPROT:Q92ZT6; UNIPARC:UPI00000CB08F; GB:AE006469; PIDN:AAK65021;
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma0684
A;Genome: plasmid
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 58.3%; Score 42; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
||| : |||
Db 92 GYWLTIW 98

RESULT 7
T42216
multidrug resistance-associated protein homolog MLP-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42216
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins m
A;Reference number: Z22081; MUID:98279126; PMID:9614210
A;Accession: T42216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1502 <HIR>
A;Cross-references: UNIPROT:O88269; UNIPARC:UPI000012F57A; EMBL:AB010466; NID:g3242457
A;Experimental source: strain Sprague-Dawley; liver

C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 58.3%; Score 42; DB 2; Length 1502;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
 |||||:
 Db 964 GYWLSLW 970

RESULT 8
 F70439
 oxaloacetate decarboxylase alpha chain - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C;Accession: F70439
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
 V.

Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: F70439
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-620 <AQF>
 A;Cross-references: UNIPROT:O67544; UNIPARC:UPI000005667F; GB:AE000747; NID:G2983944; PI
 A;Experimental source: strain VF5
 C;Genetics:

C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio
 F;540-613/Domain: lipoyl/biotin-binding homology <LPB>
 F;579/Binding site: biotin (lufs) (covalent) #status predicted

Query Match 57.6%; Score 41.5; DB 2; Length 620;
 Best Local Similarity 60.0%; Pred. No. 94;
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CGYW-LTIWG 9
 |||||:
 Db 38 CGFWSLEWVG 47

RESULT 9
 T48166
 hypothetical protein T1008.150 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: T48166
 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.
 submitted to the Protein Sequence Database, March 2000
 A;Reference number: 224486
 A;Accession: T48166
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-307 <BEV>
 A;Cross-references: UNIPROT:Q9M030; UNIPARC:UPI000009E479; EMBL:AL161746
 A;Experimental source: cultivar Columbia; BAC clone T1008
 C;Genetics:

A;Map position: 5
 A;Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1
 A;Note: T1008.150

Query Match 56.9%; Score 41; DB 2; Length 307;
 Best Local Similarity 50.0%; Pred. No. 61;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
 |||||:
 Db 186 CSFVVSIIWGC 195

RESULT 10

PC4117
 replication protein homolog - Pyrococcus sp. (fragment)
 N;Alternate names: hypothetical 391 protein
 C;Species: Pyrococcus sp.
 C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
 C;Accession: PC4117
 R;Rashid, N.; Morikawa, M.; Imanaka, T.
 Gene 166, 139-143, 1995
 A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.
 A;Reference number: JC4514; MUID:96105215; PMID:8529878
 A;Accession: PC4117
 A;Molecule type: DNA
 A;Residues: 1-391 <RAS>
 A;Cross-references: UNIPARC:UPI000017AEAF; DDBJ:D50018

Query Match 56.9%; Score 41; DB 2; Length 391;
 Best Local Similarity 85.7%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YWLTIWG 9
 |||||:
 Db 155 YWLTEWG 161

RESULT 11
 E90446
 permease [imported] - Sulfolobus solfataricus
 C;Species: Sulfolobus solfataricus
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: E90446
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
 arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A;Description: Sulfolobus solfataricus complete genome.
 A;Reference number: A99139
 A;Accession: E90446
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-419 <KUR>
 A;Cross-references: UNIPROT:Q97VB7; UNIPARC:UPI000006481C; GB:AE006641; NID:gl3816037;
 C;Genetics:
 A;Gene: SS02718

Query Match 56.9%; Score 41; DB 2; Length 419;
 Best Local Similarity 62.5%; Pred. No. 79;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9
 |||||:
 Db 365 GFWETLWG 372

RESULT 12
 T29407
 hypothetical protein C16C8.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C;Accession: T29407
 R;Waterston, R.; Le, T.T.; Gattung, S.
 submitted to the EMBL Data Library, November 1996
 A;Description: The sequence of C. elegans cosmid C16C8.
 A;Reference number: Z20617
 A;Accession: T29407
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-739 <WAT>
 A;Cross-references: UNIPARC:UPI0000175207; EMBL:U80452; PIDN:AAB37863.1; GSPDB:GN0002C
 A;Experimental source: strain Bristol N2; clone C16C8
 C;Genetics:
 A;Gene: CESP:C16C8.2
 A;Map position: 2
 A;Introns: 68/2; 179/3; 253/1; 275/3; 327/2; 365/3; 397/1; 428/2; 463/3; 629/1; 668/2;

C;Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 56.9%; Score 41; DB 2; Length 739;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
 |||: |||
 Db 118 CGFWATIREC 127

RESULT 13

sodium channel alpha subunit - long-tailed hamster (fragment)
 C;Species: Cricetulus longicaudatus (long-tailed hamster)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I48108
 R;Lalik, P.H.; Kratte, D.S.; Ciccarelli, R.B.
 Am. J. Physiol. 264, 803-809, 1993
 A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
 A;Reference number: I48107

A;Accession: I48108
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-200 <RES>
 A;Cross-references: UNIPROT:Q60464; UNIPARC:UPI00000E60A9; GB:M87541; NID:g191069; PIDN:
 C;Genetics:
 A;Gene: chol
 C;Superfamily: sodium channel protein
 C;Keywords: duplication

Query Match 56.2%; Score 40.5; DB 2; Length 200;
 Best Local Similarity 54.5%; Pred. No. 50;
 Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10
 |||: |||
 Db 26 CGEWETLWDC 36

RESULT 14

A55138
 sodium channel mRNA2.3, voltage-gated - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: A55138
 R;Felipe, A.; Knittle, T.J.; Doyle, K.L.; Tamkun, M.M.
 J. Biol. Chem. 269, 30125-30131, 1994
 A;Title: Primary structure and differential expression during development and pregnancy
 A;Reference number: A55138; MUID:95074002; PMID:7982916
 A;Accession: A55138
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1681 <FEL>
 A;Cross-references: UNIPROT:Q62467; UNIPARC:UPI0000049623; GB:L36179; NID:g609544; PIDN:
 C;Superfamily: sodium channel protein

Query Match 56.2%; Score 40.5; DB 2; Length 1681;
 Best Local Similarity 54.5%; Pred. No. 3.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10
 |||: |||
 Db 686 CGEWETLWEC 696

RESULT 15

A45380
 sodium channel protein alpha chain hNav2.1 - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: A45380
 R;George Jr., A.L.; Knittle, T.J.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992
 A;Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in hu
 A;Reference number: A45380; MUID:92279233; PMID:1317577
 A;Accession: A45380
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-1682 <GEO>
 A;Cross-references: UNIPROT:Q01118; UNIPARC:UPI00001279D2; GB:M91556; NID:g189046; PID:
 A;Experimental source: heart
 A;Note: sequence extracted from NCBI backbone (NCBIP:104344)
 C;Superfamily: sodium channel protein
 C;Keywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-ga

Query Match 56.2%; Score 40.5; DB 2; Length 1682;
 Best Local Similarity 54.5%; Pred. No. 3.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10
 |||: |||
 Db 686 CGEWETLWDC 696

Search completed: May 2, 2006, 08:56:21
 Job time : 19.1395 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 113.256 Seconds

(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	63.9	218	1 Y232 SYNY3	Q55705 synchocyst
2	45.5	63.2	173	2 Q4Y1C8 PLACH	Q4Y1C8 plasmidum
3	45	62.5	360	2 Q67Q12 SYMTH	Q67Q12 symbiobacte
4	45	62.5	828	2 Q8ZBL4 YERPE	Q8ZBL4 versinia pe
5	45	62.5	828	2 Q66EF6 YERPE	Q66EF6 versinia ps
6	45	62.5	853	2 Q8DIA7 YERPE	Q8DIA7 versinia pe
7	43.5	60.4	1993	2 P90670 APLCA	P90670 aplysia cal
8	43	59.7	168	2 Q6H022 FREDI	Q6H022 fremyella d
9	43	59.7	215	2 Q57Z63 TRYVP	Q57Z63 trypanosoma
10	43	59.7	220	2 Q4QID2 LEIMA	Q4QID2 leishmania
11	43	59.7	221	2 Q74JK6 LACJO	Q74JK6 lactobacill
12	43	59.7	454	2 Q59NK9 CANAL	Q59NK9 candida alb
13	43	59.7	501	2 Q6C574 YARLI	Q6C574 yarrowia li
14	43	59.7	520	2 Q4XP68 PLACH	Q4XP68 plasmidum
15	43	59.7	645	2 Q8DKD6 SYNEL	Q8DKD6 synchococc
16	43	59.7	733	2 Q8H2N7 ORYSA	Q8H2N7 oryza sativ
17	43	59.7	1084	2 Q7WY20 PSEAE	Q7WY20 pseudomonas
18	42.5	59.0	152	1 ATRAP FONPY	Q3rer2 pongo pygma
19	42.5	59.0	159	1 ATRAP HUMAN	Q6rwl3 homo sapien
20	42.5	59.0	263	2 Q7YVFI CRYPV	Q7YVFI cryptospori
21	42.5	59.0	263	2 Q5CN44 CRVHO	Q5CN44 cryptospori
22	42.5	59.0	1765	1 SC11A RAT	Q88457 rattus norv
23	42	58.3	72	1 VG35 BPMLS	Q85245 mycobacteri
24	42	58.3	133	2 Q855L3 9CAUD	Q855L3 mycobacteri
25	42	58.3	284	2 Q6MC01 PARUW	Q6MC01 parachlamyd
26	42	58.3	314	2 Q4NT43 9DELT	Q4NT43 anaeromyxob
27	42	58.3	343	2 Q94FS2 CAJCA	Q94fs2 cajanus caj
28	42	58.3	389	2 Q8J151 TROW8	Q8J151 tropheryma
29	42	58.3	441	2 Q92Z76 RHIME	Q92zt6 rhizobium m
30	42	58.3	452	2 Q83G14 TROWT	Q83G14 tropheryma
31	42	58.3	472	1 RBL_NITVU	Q59613 nitrobacter

32	42	58.3	473	2 Q8VQ84 9PROT	Q8vq84 nitrospir
33	42	58.3	473	2 Q9XD76 NITWI	Q9xd76 nitrobacter
34	42	58.3	473	2 Q9XD77 NITWI	Q9xd77 nitrobacter
35	42	58.3	1308	2 Q8T6H2 DICDI	Q8t6h2 dictyosteli
36	42	58.3	1328	2 Q54EK2 DICDI	Q54ek2 dictyosteli
37	42	58.3	1498	1 MRP6 MUSE	Q9rls7 mus musculu
38	42	58.3	1502	1 MRP6 RAT	Q88269 rattus norv
39	42	58.3	1503	1 MRP6 HUMAN	Q95255 homo sapien
40	41.5	57.6	122	2 Q8N125 HUMAN	Q8n125 homo sapien
41	41.5	57.6	473	2 Q5T2N8 HUMAN	Q5t2n8 homo sapien
42	41.5	57.6	620	2 Q67544 AQUAE	Q67544 aquifex aeo
43	41	56.9	266	2 Q82285 ENTFA	Q82285 enterococcu
44	41	56.9	307	2 Q9M030 ARATH	Q9m030 arabidopsis
45	41	56.9	376	1 ETR1 YARLI	Q6cbe4 yarrowia li

ALIGNMENTS

RESULT 1
Y232_SYNY3
ID Y232 SYNY3 STANDARD; PRT; 218 AA.
AC Q55705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein slr0232.
GN OrderedLocustNames=slr0232;
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Suglura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Suglura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- SIMILARITY: Belongs to the deda family.

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between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

CC EMBL; BA000022; BAA10237.1; -; Genomic_DNA.
CC PIR; S76385; S76385.
CC InterPro; IPR000252; Deda.
CC Pfam; PF00597; Deda; 1.
CC Complete proteome; Hypothetical protein.
SQ SEQUENCE 218 AA; 23782 MW; C04B5D7B7EA7F863 CRC64;

Query Match 63.9%; Score 46; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9

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Db      73 CGYVWGRWG 81
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SQ SEQUENCE 360 AA; 39433 MW; EEB0B58F939CE443 CRC64;
Query Match 62.5%; Score 45; DB 2; Length 360;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
Q4Y1C8_PLACH PRELIMINARY; PRT; 173 AA.
AC Q4Y1C8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PC103204.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01001794; CAH7032.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 173 AA; 21349 MW; 053E43204D83013F CRC64;

Query Match 63.28; Score 45.5; DB 2; Length 173;
Best Local Similarity 72.7%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CGYWLFTIW 8
||||: |||
DB 12 CGYWLFEKTIW 22

RESULT 3
Q67012_SYMPH PRELIMINARY; PRT; 360 AA.
AC Q67012;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=STH1076;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
NUCLEOTIDE SEQUENCE.
RA STRAIN=T / IAM 14863;
RA PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yanashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AP006840; BAD40061.1; -; Genomic DNA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase M23B.
DR Pfam; PF01551; Peptidase M23; I.
KW Complete proteome; Copper; Hypothetical protein; Metal-binding;
KW Oxidoreductase.

SQ SEQUENCE 360 AA; 39433 MW; EEB0B58F939CE443 CRC64;
Query Match 62.5%; Score 45; DB 2; Length 828;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTIWGC 10
||||: |||
DB 372 CGLWLELLSWGC 383

RESULT 5
Q66EF6_YERPS PRELIMINARY; PRT; 828 AA.
ID Q66EF6_YERPS
AC Q66EF6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

SQ SEQUENCE 828 AA; 91983 MW; 3A1F8883D5D5E583 CRC64;
Query Match 62.5%; Score 45; DB 2; Length 828;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTIWGC 10
||||: |||
DB 372 CGLWLELLSWGC 383

RESULT 4
Q8ZBL4_YERPE PRELIMINARY; PRT; 828 AA.
ID Q8ZBL4_YERPE
AC Q8ZBL4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ATP-dependent helicase.
GN Name=hrpB; OrderedLocusNames=YPO3394;
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
NUCLEOTIDE SEQUENCE.
RA STRAIN=CO-92 / Biovar Orientalis;
RA MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RA "Genome sequence of Versinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414156; CAC92624.1; -; Genomic_DNA.
DR PIR; AD0412; AD0412.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR010225; DEAH_box_HrpB.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR PIRSF; PIRSF005496; ATP_hel_hrpB; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR TIGRfams; TIGR01970; DEAH_box_HrpB; 1.
KW ATP-binding; Complete proteome; Helicase; Hydrolase.
SQ SEQUENCE 828 AA; 91983 MW; 3A1F8883D5D5E583 CRC64;

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Tue May 2 12:32:40 2006

us-10-046-922-35.rup

25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Helicase, ATP-dependent.
 GN Name-hrp, Synonyms-yado; OrderedLocusNames=YPTB0737;
 OS Yersinia pseudotuberculosis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OX Enterobacteriaceae; Yersinia.
 NCBI_TaxID=633;
 [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=IP32953 / Serotype I;
 RC PubMed=15358858; DOI=10.1073/pnas.0404012101;
 RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regalia W.M., Georges A.M., Vergez L.M., Land M.L., Motin V.L.,
 RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
 RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser L.J., Garcia E.;
 RT "Insights into the evolution of Yersinia pestis through whole-genome
 comparison with Yersinia pseudotuberculosis";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 DR EMBL: BX936398; CAH19977.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO: GO:0016787; F:Hydrolase activity; IEA.
 DR GO: GO:0003676; F:Nucleic acid binding; IEA.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR010225; DEAH_box_HrpB.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR007502; Helicase_dom.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF04408; HA2; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR PIRSF: PIRSF005496; ATP_hel_hrpB; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR TIGRFAMS: TIGR01970; DEAH_box_HrpB; 1.
 DR ATP-binding; Complete proteome; Helicase; Hydrolase.
 KW SEQUENCE 828 AA; 91983 MW; CF11PDD863330635 CRC64;
 SQ
 Query Match 62.5%; Score 45; DB 2; Length 828;
 Best Local Similarity 58.3%; Pred. No. 2.8e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 QY 1 CGWLTII--WGC 10
 DB 372 CGLWLELLSWGC 383
 RESULT 6
 Q8DIA7_YERPE
 ID Q8DIA7_YERPE PRELIMINARY; PRT; 853 AA.
 AC Q8DIA7_Y4XU2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Helicase, ATP-dependent.
 GN Name-hrp; OrderedLocusNames=YPT0291, Y0794;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=KIMS / Biovar Mediaevalis;
 RC MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM";
 RL J. Bacteriol. 184:4601-4611(2002).

[2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=91001;
 RC PubMed=15368893;
 RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
 RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
 RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
 RA Yang H., Wang J., Huang P., Yang R.;
 RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
 avirulent to humans";
 RL DNA Res. 11:179-197(2004).
 DR EMBL: AE013681; AAM84381.1; -; Genomic DNA.
 DR EMBL: AE017128; AAS60566.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO: GO:0016787; F:Hydrolase activity; IEA.
 DR GO: GO:0003676; F:Nucleic acid binding; IEA.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR010225; DEAH_box_HrpB.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR007502; Helicase_dom.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF04408; HA2; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR PIRSF: PIRSF005496; ATP_hel_hrpB; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR TIGRFAMS: TIGR01970; DEAH_box_HrpB; 1.
 DR ATP-binding; Helicase; Hydrolase.
 KW SEQUENCE 853 AA; 95005 MW; B3DB738A18665B42 CRC64;
 SQ
 Query Match 62.5%; Score 45; DB 2; Length 853;
 Best Local Similarity 58.3%; Pred. No. 2.8e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 QY 1 CGWLTII--WGC 10
 DB 397 CGLWLELLSWGC 408
 RESULT 7
 P90670_APLCA
 ID P90670_APLCA PRELIMINARY; PRT; 1993 AA.
 AC P90670;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Sodium channel alpha-subunit SCAP1.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidaea;
 OC Aplysioidae; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Nervous system;
 RC MEDLINE=97238630; PubMed=9115644;
 RX Dyer J.R., Johnston W.L., Castellucci V.F., Dunn R.J.;
 RT "Cloning and tissue distribution of the Aplysia Na+ channel alpha-
 subunit cDNA";
 RL DNA Cell Biol. 16:347-356(1997).
 DR EMBL: U66915; AAC47457.1; -; mRNA.
 DR PIR: T30902; T30902.
 DR HSP: P04775; 1BY.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO: GO:0005261; F:cation channel activity; IEA.
 DR GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO: GO:0006812; P:cation transport; IEA.
 DR GO: GO:0006814; P:sodium ion transport; IEA.
 DR InterPro: IPR001682; Ca/Na_pore.

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DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
KW Ion transport; Ionic channel; Sodium channel; Sodium transport;
KW Transmembrane; Transport; Voltage-gated channel.
SQ SEQUENCE 1993 AA; 225896 MW; 33E174B9BF07E1A7 CRC64;

Query Match 60.4%; Score 43.5; DB 2; Length 1993;
Best Local Similarity 54.5%; Pred. No. 1e+03;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TWGC 10
DB 942 CGEWLSWGC 952
|||||
Query Match 59.7%; Score 43; DB 2; Length 215;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
Q6H022_FREDI PRELIMINARY; PRT; 168 AA.
ID Q6H022_FREDI
AC Q6H022;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Microchaete.
OX NCBI_TaxID=1197;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FD33;
RA Stowe-Evans E.L., Ford J., Kehoe D.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL; AY548455; AAT41947.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 168 AA; 18932 MW; 1C9DB963D5210332 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 168;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYWL-TWGC 9
DB 122 CGYWLSDRG 130
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Query Match 59.7%; Score 43; DB 2; Length 220;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
Q74JK6_LACJO PRELIMINARY; PRT; 221 AA.
ID Q74JK6_LACJO
AC Q74JK6;
DT 05-JUL-2004 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Tb27.5.3300;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;

RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Fai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Haas B., Blandin G., El-Sayed N.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC113585; AAX79570.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 215 AA; 25574 MW; C32B79363DCDC6A CRC64;

Query Match 59.7%; Score 43; DB 2; Length 215;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTWGC 10
DB 123 WYTLWGC 129
|||||
Query Match 59.7%; Score 43; DB 2; Length 220;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
Q4QID2_LEIMA PRELIMINARY; PRT; 220 AA.
ID Q4QID2_LEIMA
AC Q4QID2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF08.0370;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivans A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT05247; CAJ02216.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 220 AA; 26176 MW; 3AB510340D9F5583 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 220;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTWGC 10
DB 128 WYTLWGC 134
|||||
Query Match 59.7%; Score 43; DB 2; Length 221 AA.
ID Q74JK6_LACJO PRELIMINARY; PRT; 221 AA.
AC Q74JK6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN OrderedLocustNames=LJ1101;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
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DB 137 YWLTGWSC 144

NCBI_TaxID=33959;
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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RX PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Pridmore R.D., Barger B., Desiere F., Villanova D., Barretto C.,
RA Pittet A.-C., Zechlen M.-C., Rouvet M., Altermann E., Barranger R.,
RA Mollat B., Mercenier A., Klammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT *Lactobacillus johnsonii* NCC 533";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
DR EMBL: AE017203; RAS08923.1; -: Genomic DNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019835; P: cytolysis; IEA.
DR InterPro: IPR004254; HlyVIII related.
DR Pfam: PF03006; HlyVIII; 1.
DR TIGRFAMs: TIGR01065; hlyVIII; 1.
DR Complete proteome.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
Query Match 59.7%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
172 GFWLLVWG 179

DB 172 GFWLLVWG 179

RESULT 12
Q59NK9 CANAL PRELIMINARY; PRT; 454 AA.
ID Q59NK9
AC Q59NK9
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
DE ORFNames=Ca019.6606;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
ON NCBI_TaxID=237561;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
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RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[2]
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RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
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RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[2]
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RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
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RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
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RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[1]
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RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
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RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[1]
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RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
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RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314.

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAJ01004254; CAH81294.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 520 AA; 52230 MW; 08E31B477FEFD368 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 520;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GYWLTING 9
DB 167 GYWLNSWG 174

RESULT 15

Q8DKD6_SYNEL
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AC Q8DKD6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T110923 protein.
GN OrderedLocusNames=t110923;
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iiguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RL Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; BA000039; BAC08475.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2CC; 1.
DR SMART; SM00331; PP2C_SIG; 1.
KW Complete proteome.
SQ SEQUENCE 646 AA; 71071 MW; 56CSA74F76652D56 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 646;
Best Local Similarity 62.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 YMLTINGC 10
DB 415 YWINRWGC 422

Search completed: May 2, 2006, 08:46:50
Job time : 115.256 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 28.3721 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	61.8	1024	US-09-562-737-84	Sequence 84, Appl
2	43	59.7	492	US-09-107-532A-6945	Sequence 6945, Ap
3	42.5	59.0	1024	US-09-562-737-86	Sequence 86, Appl
4	42.5	59.0	1765	US-09-354-147C-2	Sequence 2, Appli
5	42.5	59.0	1765	US-09-354-147C-3	Sequence 3, Appli
6	42	58.3	161	US-09-325-932A-187	Sequence 187, App
7	42	58.3	273	US-09-270-767-46926	Sequence 46926, A
8	42	58.3	1498	US-09-792-616-9	Sequence 9, Appli
9	42	58.3	1503	US-09-792-616-3	Sequence 3, Appli
10	42	58.3	1503	US-09-647-140B-8	Sequence 8, Appli
11	41	56.9	222	US-09-071-035-408	Sequence 408, App
12	41	56.9	222	US-10-206-576-408	Sequence 408, App
13	41	56.9	229	US-09-134-000C-3630	Sequence 3630, Ap
14	41	56.9	264	US-09-540-236-2978	Sequence 2978, Ap
15	41	56.9	266	US-09-071-035-406	Sequence 406, App
16	41	56.9	266	US-10-206-576-406	Sequence 406, App
17	40.5	56.2	1024	US-09-562-737-81	Sequence 81, Appl
18	40.5	56.2	1024	US-09-562-737-87	Sequence 87, Appl
19	40.5	56.2	1255	US-09-949-016-10988	Sequence 10988, A
20	40.5	56.2	1681	US-09-920-653B-3	Sequence 3, Appli
21	40.5	56.2	1835	US-08-836-325-15	Sequence 15, Appl
22	40.5	56.2	1835	US-09-457-571-15	Sequence 15, Appl
23	40.5	56.2	1836	US-10-162-012-24	Sequence 24, Appl
24	40.5	56.2	1836	US-08-836-325-16	Sequence 16, Appl
25	40.5	56.2	1969	US-09-457-571-16	Sequence 16, Appl
26	40.5	56.2	1976	US-09-024-020B-9	Sequence 9, Appli
27	40.5	56.2	1976	US-09-425-043-9	Sequence 9, Appli

28	40.5	56.2	1977	2	US-09-976-594-757	Sequence 757, App
29	40.5	56.2	1977	2	US-09-919-039-367	Sequence 367, App
30	40.5	56.2	1978	2	US-09-024-020B-3	Sequence 3, Appli
31	40.5	56.2	1978	2	US-09-425-043-3	Sequence 3, Appli
32	40.5	56.2	1984	2	US-08-836-325-10	Sequence 10, Appl
33	40.5	56.2	1984	2	US-09-457-571-10	Sequence 10, Appl
34	40.5	56.2	1988	2	US-09-024-020B-4	Sequence 4, Appli
35	40.5	56.2	1988	2	US-09-425-043-4	Sequence 4, Appli
36	40.5	56.2	1989	2	US-08-836-325-11	Sequence 11, Appl
37	40.5	56.2	1989	2	US-08-836-325-12	Sequence 12, Appl
38	40.5	56.2	1989	2	US-09-457-571-11	Sequence 11, Appl
39	40.5	56.2	1989	2	US-09-457-571-12	Sequence 12, Appl
40	40.5	56.2	1989	2	US-09-949-016-10076	Sequence 10076, A
41	40.5	56.2	2005	2	US-08-836-325-7	Sequence 7, Appli
42	40.5	56.2	2005	2	US-09-457-571-7	Sequence 7, Appli
43	40.5	56.2	2016	2	US-09-634-920-4	Sequence 4, Appli
44	40.5	56.2	2016	2	US-09-514-907A-2	Sequence 2, Appli
45	40.5	56.2	2016	2	US-09-896-994-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-562-737-84
; Sequence 84, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-84

Query Match 61.8%; Score 44.5; DB 2; Length 1024;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 CGYWL-TWGC 10
|||:|:|:
Db 892 CGHWIETWDC 902

RESULT 2
US-09-107-532A-6945
; Sequence 6945, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC

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/ OPERATING SYSTEM: <Unknown>
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/107,532A
/   FILING DATE: 30-Jun-1998
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: 60/085,598
/   FILING DATE: 14 May 1998
/   APPLICATION NUMBER: 60/051571
/   FILING DATE: July 2, 1997
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Ariniello, Pamela Deneke
/   REGISTRATION NUMBER: 40,489
/   REFERENCE/DOCKET NUMBER: GTC-012
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (781)893-5007
/   TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 6945:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 492 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/   ORGANISM: Enterococcus faecium
/ FEATURE:
/   NAME/KEY: misc feature
/   LOCATION: (B) LOCATION 1...492
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945

Query Match          59.7%; Score 43; DB 2; Length 492;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
DB      112 GYWLTCW 118

RESULT 3
US-09-562-737-86
/ Sequence 86, Application US/09562737
/ Patent No. 6428967
/ GENERAL INFORMATION:
/   APPLICANT: Herz, Joachim
/   TITLE OF INVENTION: LDL Receptor Signaling Pathways
/   FILE REFERENCE: UTSW0708
/   CURRENT APPLICATION NUMBER: US/09/562,737
/   CURRENT FILING DATE: 2000-05-01
/   NUMBER OF SEQ ID NOS: 132
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 86
/   LENGTH: 1024
/   TYPE: PRT
/   ORGANISM: Artificial Sequence
/ FEATURE:
/   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-86

Query Match          59.0%; Score 42.5; DB 2; Length 1024;
Best Local Similarity 63.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
DB      892 CGEWLETWDC 902

RESULT 4
US-09-354-147C-2
/ Sequence 2, Application US/09354147C
/ Patent No. 6573067
/ GENERAL INFORMATION:
/   APPLICANT: Dib-Hajj, Sulayman
/   TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
/   FILE REFERENCE: 44574-5004-01-US
/   CURRENT APPLICATION NUMBER: US/09/354,147C
/   CURRENT FILING DATE: 1999-07-16
/   PRIOR APPLICATION NUMBER: US 60/072,990
/   PRIOR FILING DATE: 1998-01-29
/   PRIOR APPLICATION NUMBER: US 60/109,402
/   PRIOR FILING DATE: 1998-11-20
/   PRIOR APPLICATION NUMBER: PCT/US99/02008
/   PRIOR FILING DATE: 1999-01-29
/   NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/   LENGTH: 1765
/   TYPE: PRT
/   ORGANISM: Rattus norvegicus
/ FEATURE:
/   NAME/KEY: UNSURE
/   LOCATION: (652)...(1334)
/   OTHER INFORMATION: Xaa at position 652 is Leu; Xaa at position 1334 is Asn
/   OTHER INFORMATION: or Lys. Xaa's result from n's in SEQ ID NO: 1.
US-09-354-147C-2

Query Match          59.0%; Score 42.5; DB 2; Length 1765;
Best Local Similarity 54.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
DB      754 CGEWIENWGC 764

RESULT 5
US-09-354-147C-3
/ Sequence 3, Application US/09354147C
/ Patent No. 6573067
/ GENERAL INFORMATION:
/   APPLICANT: Dib-Hajj, Sulayman
/   TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
/   FILE REFERENCE: 44574-5004-01-US
/   CURRENT APPLICATION NUMBER: US/09/354,147C
/   CURRENT FILING DATE: 1999-07-16
/   PRIOR APPLICATION NUMBER: US 60/072,990
/   PRIOR FILING DATE: 1998-01-29
/   PRIOR APPLICATION NUMBER: US 60/109,402
/   PRIOR FILING DATE: 1998-11-20
/   PRIOR APPLICATION NUMBER: PCT/US99/02008
/   PRIOR FILING DATE: 1999-01-29
/   NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/   LENGTH: 1765
/   TYPE: PRT
/   ORGANISM: Rattus norvegicus
/ FEATURE:
/   OTHER INFORMATION: putative amino acid seq. of rat Nan
US-09-354-147C-3

Query Match          59.0%; Score 42.5; DB 2; Length 1765;
Best Local Similarity 54.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
DB      754 CGEWIENWGC 764
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match 58.3%; Score 42; DB 2; Length 1498;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
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Db 960 GYWLSLW 966

RESULT 9
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: PXE-001 Pseudoxanthoma Elasticum
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match 58.3%; Score 42; DB 2; Length 1503;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
   |||::|
Db 965 GYWLSLW 971

RESULT 10
US-09-647-140B-8
; Sequence 8, Application US/09647140B
; Patent No. 6803184
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun.
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
; FILE REFERENCE: FCCC 98-02 Nucleic Acids and Methods of Use Thereof
; CURRENT APPLICATION NUMBER: US/09/647,140B
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US99/066644
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,759
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/095,153
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-647-140B-8

Query Match 58.3%; Score 42; DB 2; Length 1503;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;

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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
Db 965 GYWLTLW 971

RESULT 11
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-071-035-408

Query Match 56.9%; Score 41; DB 2; Length 222;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
Db 179 GTWITLW 186

RESULT 12
US-10-206-576-408
; Sequence 408, Application US/10206576
; Patent No. 6913907
; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA

Query Match 56.9%; Score 41; DB 2; Length 229;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
Db 203 GTWITLW 210

RESULT 14

ZIP: 20850
COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: Dell Latitude
; OPERATING SYSTEM: Windows 98
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,576
; FILING DATE: 29-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/071,035
; FILING DATE: 1998-05-04
; APPLICATION NUMBER: US 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: US 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: US 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Mark J.
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB369P1D1
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 408:
; US-10-206-576-408

Query Match 56.9%; Score 41; DB 2; Length 222;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
Db 179 GTWITLW 186

RESULT 13
US-09-134-000C-3630
; Sequence 3630, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3630
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-3630

Query Match 56.9%; Score 41; DB 2; Length 229;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
Db 203 GTWITLW 210

RESULT 14

US-09-540-236-2978
; Sequence 2978, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2978
; LENGTH: 264
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2978

Query Match 56.9%; Score 41; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8
DB 200 CGAWLGIW 207

RESULT 15
US-09-071-035-406
; Sequence 406, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 406:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-406

Query Match 56.9%; Score 41; DB 2; Length 266;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
DB 203 GTWITLW 210

Search completed: May 2, 2006, 08:58:27
Job time : 29.3721 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 93.0233 Seconds
(without alignments)
44.917 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	54	75.0	10	4	US-10-046-922-34
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4	47.5	66.0	304	4	US-10-017-161-2288
5	47.5	66.0	304	4	US-10-292-798-1934
6	47	65.3	25	4	US-10-280-066-476
7	47	65.3	63	4	US-10-437-963-125253
8	46	63.9	17	4	US-10-125-869A-54
9	46	63.9	17	4	US-10-462-262-278
10	46	63.9	136	4	US-10-112-944-743
11	45	62.5	828	4	US-10-282-122A-77862
12	44.5	61.8	1024	4	US-10-211-962-84
13	44	61.1	103	4	US-10-437-963-181150
14	44	61.1	112	5	US-10-981-738-1
15	44	61.1	119	5	US-10-981-738-30
16	44	61.1	119	5	US-10-981-738-32
17	44	61.1	119	5	US-10-981-738-34
18	44	61.1	119	5	US-10-981-738-36
19	44	61.1	119	5	US-10-981-738-38
20	44	61.1	119	5	US-10-981-738-40
21	44	61.1	119	5	US-10-981-738-42
22	44	61.1	119	5	US-10-981-738-44
23	44	61.1	119	5	US-10-981-738-46
24	44	61.1	119	5	US-10-981-738-48
25	44	61.1	119	5	US-10-981-738-50
26	44	61.1	119	5	US-10-981-738-52
27	44	61.1	119	5	US-10-981-738-54

28	44	61.1	119	5	US-10-981-738-56	Sequence 56, Appl
29	44	61.1	119	5	US-10-981-738-58	Sequence 58, Appl
30	44	61.1	119	5	US-10-981-738-60	Sequence 60, Appl
31	44	61.1	119	5	US-10-981-738-62	Sequence 62, Appl
32	44	61.1	119	5	US-10-981-738-64	Sequence 64, Appl
33	44	61.1	119	5	US-10-981-738-66	Sequence 66, Appl
34	44	61.1	119	5	US-10-981-738-68	Sequence 68, Appl
35	44	61.1	119	5	US-10-981-738-70	Sequence 70, Appl
36	44	61.1	119	5	US-10-981-738-72	Sequence 72, Appl
37	44	61.1	161	4	US-10-767-701-54778	Sequence 54778, A
38	44	61.1	468	5	US-10-981-738-13	Sequence 13, Appl
39	43	59.7	13	4	US-10-125-869A-73	Sequence 297, App
40	43	59.7	13	4	US-10-462-262-297	Sequence 297, App
41	43	59.7	291	4	US-10-369-493-19313	Sequence 19313, A
42	43	59.7	454	4	US-10-032-585-7816	Sequence 7816, Ap
43	43	59.7	459	4	US-10-437-963-160191	Sequence 160191, A
44	43	59.7	474	4	US-10-282-122A-57928	Sequence 57928, A
45	43	59.7	671	4	US-10-437-963-190740	Sequence 190740, A

ALIGNMENTS

RESULT 1
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match 100.0%; Score 72; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
Db 1 CGYWLTIWGC 10

RESULT 2
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; NAME/KEY: SITE
; LOCATION: (1)...(1)

; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match 75.0%; Score 54; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9
Db 2 GYWLTIWG 9

RESULT 3
US-10-046-922-73
; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 10
; TYPE: PRT
; ORGANISM: peptide library
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(7)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-73

Query Match 69.4%; Score 50; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.9;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
Db 1 CGYWXWXC 10

RESULT 4
US-10-017-161-2288
; Sequence 2288, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2288
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: MOD RES
; LOCATION: (73)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (79)..(83)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (85)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (89)..(91)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (96)..(97)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (101)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (107)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (118)..(119)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (121)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (123)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (162)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (178)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (194)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (210)..(211)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (219)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-2288

Query Match 66.0%; Score 47.5; DB 4; Length 304;
Best Local Similarity 60.0%; Pred. No. 1e-02; Mismatches 1; Indels 1; Gaps 1;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CGYWLTIWGC 10
Db 108 CGFW-AWGC 116

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RESULT 5
US-10-292-798-1934
; Sequence 1934, Application US/10292798
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1934
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (73)..(73)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (80)..(83)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (89)..(91)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (96)..(97)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (101)..(101)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (107)..(107)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (118)..(119)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (121)..(121)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (123)..(123)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (178)..(178)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (210)..(211)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (219)..(219)
; OTHER INFORMATION: Variable amino acid
; FEATURE:

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; NAME/KEY: MOD_RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-292-798-1934
Query Match
Best Local Similarity 66.0%; Score 47.5; DB 4; Length 304;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 CGYWLTIWGC 10
Db 108 CGFW-AVWGC 116
RESULT 6
US-10-280-066-476
; Sequence 476, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BI
; FILE REFERENCE: 2598-4009US1
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 476
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Tie1-20C-3-D116
US-10-280-066-476
Query Match
Best Local Similarity 65.3%; Score 47; DB 4; Length 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGYWLTIW 9
Db 5 CGYWGELNG 13
RESULT 7
US-10-437-963-125253
; Sequence 125253, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 125253
; LENGTH: 63

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; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27915C.1.pep
US-10-437-963-125253

Query Match      65.3%; Score 47; DB 4; Length 63;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
   |||:| |||
Db 37 CGHYLKAWGC 46

RESULT 8
US-10-125-869A-54
; Sequence 54, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-54

Query Match      63.9%; Score 46; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9
   |||:| |||
Db 4 CGFWPRIMG 12

RESULT 9
US-10-462-262-278
; Sequence 278, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
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US-10-462-262-278

Query Match      63.9%; Score 46; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9
   |||:| |||
Db 4 CGFWPRIMG 12

RESULT 10
US-10-112-944-743
; Sequence 743, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 743
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(136)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set f
; OTHER INFORMATION: in Example 2
US-10-112-944-743

Query Match      63.9%; Score 46; DB 4; Length 136;
Best Local Similarity 60.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
   |||:| |||
Db 93 CGRWDWLWGC 102

RESULT 11
US-10-282-122A-77862
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Sequence 77862, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 77862
 LENGTH: 828
 TYPE: PRT
 ORGANISM: Yersinia pestis
 US-10-282-122A-77862

Query Match 62.5%; Score 45; DB 4; Length 828;
 Best Local Similarity 58.3%; Pred. No. 5e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYMLTI--WGC 10
 DB 372 CGLMLELLSWGC 383

RESULT 12

US-10-211-962-84

Sequence 84, Application US/10211962

Publication No. US20030082640A1

GENERAL INFORMATION:

APPLICANT: Herz, Joachim

APPLICANT: Gotthardt, Michael

TITLE OF INVENTION: LDL Receptor Signaling Pathways

FILE REFERENCE: UTSW0708

CURRENT APPLICATION NUMBER: US/10/211,962

CURRENT FILING DATE: 2002-08-01

PRIOR APPLICATION NUMBER: US/09/562,737

PRIOR FILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 132

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 1024

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

US-10-211-962-84

Query Match 61.8%; Score 44.5; DB 4; Length 1024;
 Best Local Similarity 54.5%; Pred. No. 7e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYML-TIWGC 10
 DB 892 CGHWIETWDC 902

RESULT 13

US-10-437-963-181150

Sequence 181150, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 181150

LENGTH: 103

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT MRT4530_78451C.1.pep

US-10-437-963-181150

Query Match 61.1%; Score 44; DB 4; Length 103;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 YMLTIWGC 10
 DB 19 WWVSVWGC 26

RESULT 14

US-10-981-738-1

Sequence 1, Application US/10981738

Publication No. US20050123546A1

GENERAL INFORMATION:

APPLICANT: Umana, Pablo

APPLICANT: Bruenker, Peter

APPLICANT: Suter, Tobias

APPLICANT: Puenteener, Ursula

APPLICANT: Moessner, Ekkehard

APPLICANT: Ferrara, Claudia

TITLE OF INVENTION: Antigen Binding Molecules with Increased Fc Receptor Binding

FILE REFERENCE: 1975.0290001

CURRENT APPLICATION NUMBER: US/10/981,738

CURRENT FILING DATE: 2004-11-05

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1

LENGTH: 112

; TYPE: PRT
; ORGANISM: Mus sp.
US-10-981-738-1

Query Match 61.1%; Score 44; DB 5; Length 112;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTIWG 9
| | | | |
Db 96 GYWLVIWG 103

RESULT 15
US-10-981-738-30
; Sequence 30, Application US/10981738
; Publication No. US20050123546A1
; GENERAL INFORMATION:
; APPLICANT: Umana, Pablo
; APPLICANT: Bruenker, Peter
; APPLICANT: Suter, Tobias
; APPLICANT: Puenteener, Ursula
; APPLICANT: Moessner, Ekkehard
; APPLICANT: Ferrara, Claudia
; TITLE OF INVENTION: Antigen Binding Molecules with Increased Fc Receptor Binding
; TITLE OF INVENTION: Affinity and Effector Function
; FILE REFERENCE: 1975.0290001
; CURRENT APPLICATION NUMBER: US/10/981,738
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mouse-human chimeric polypeptide
US-10-981-738-30

Query Match 61.1%; Score 44; DB 5; Length 119;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTIWG 9
| | | | |
Db 103 GYWLVIWG 110

Search completed: May 2, 2006, 09:32:40
Job time : 94.0233 secs

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OM protein - protein search, using sw_model

Run on: May 2, 2006, 09:26:17 ; Search time 14.186 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGWLLTWGC 10

Scoring table: BLOSUM62

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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6: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
8: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
10: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42.5	59.0	152	11	US-11-264-096-1533
2	42.5	59.0	159	11	US-11-264-096-1534
3	42.5	58.3	441	11	US-11-087-099-2305
4	42.5	58.3	1023	9	US-10-995-561-968
5	41	56.9	395	11	US-11-124-367A-322
6	41	56.9	432	11	US-11-124-367A-326
7	41	56.9	637	11	US-11-124-367A-321
8	40.5	56.2	268	11	US-11-096-568A-19834
9	40.5	56.2	1981	9	US-10-374-954-23
10	40.5	56.2	1998	9	US-10-374-954-21
11	40.5	56.2	2009	9	US-10-374-954-2
12	40	55.6	10	11	US-11-129-741-3641
13	40	55.6	119	11	US-11-250-411-97
14	40	55.6	119	11	US-11-250-411-101
15	40	55.6	138	11	US-11-250-411-86
16	40	55.6	138	11	US-11-250-411-90
17	40	55.6	167	11	US-11-236-198-33
18	39.5	54.9	174	11	US-11-188-298-2376
19	39	54.2	257	11	US-11-087-099-983
20	39	54.2	318	11	US-11-087-099-6672
21	39	54.2	342	11	US-11-087-099-2365

22	39	54.2	401	11	US-11-096-568A-25197	Sequence 25197, A
23	39	54.2	419	11	US-11-096-568A-25196	Sequence 25196, A
24	39	54.2	433	11	US-11-087-099-567	Sequence 567, App
25	39	54.2	450	11	US-11-096-568A-25195	Sequence 25195, A
26	39	54.2	454	11	US-11-087-099-4113	Sequence 4113, Ap
27	39	54.2	471	11	US-11-188-298-19864	Sequence 19864, A
28	39	54.2	475	11	US-11-188-298-5764	Sequence 5764, Ap
29	39	54.2	476	11	US-11-087-099-1256	Sequence 1256, Ap
30	39	54.2	478	11	US-11-087-099-9555	Sequence 9555, Ap
31	39	54.2	478	11	US-11-188-298-8872	Sequence 8872, Ap
32	39	54.2	478	11	US-11-188-298-8872	Sequence 217, App
33	38.5	53.5	18	11	US-11-233-256-217	Sequence 217, App
34	38.5	53.5	18	11	US-11-233-256-217	Sequence 5844, Ap
35	38.5	53.5	458	11	US-11-087-099-5844	Sequence 5844, Ap
36	38	52.8	253	11	US-11-096-568A-7538	Sequence 7538, Ap
37	38	52.8	322	11	US-11-087-099-2014	Sequence 2014, Ap
38	38	52.8	349	11	US-11-188-298-17452	Sequence 17452, A
39	38	52.8	363	9	US-10-444-926-10	Sequence 10, Appl
40	38	52.8	382	9	US-10-444-926-8	Sequence 8, Appl
41	38	52.8	387	9	US-10-444-926-14	Sequence 14, Appl
42	38	52.8	389	11	US-11-096-568A-8051	Sequence 8051, Ap
43	38	52.8	391	11	US-11-127-877-52	Sequence 52, Appl
44	38	52.8	400	11	US-11-096-568A-7537	Sequence 7537, Ap
45	38	52.8	415	9	US-10-444-926-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-11-264-096-1533
; Sequence 1533, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264, 096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1533
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1533

Query Match 59.0%; Score 42.5; DB 11; Length 152;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 2 GYW-LTIWGC 10

Db 14 GHWLLTWGC 23

RESULT 2

US-11-264-096-1534
; Sequence 1534, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264, 096

0:

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QY      2 GYWLTIWGC 10
Db      20 GINFLWGC 28

RESULT 7
US-11-124-367A-321
; Sequence 321, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-321

Query Match      56.9%; Score 41; DB 11; Length 637;
Best Local Similarity 55.6%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

QY      2 GYWLTIWGC 10
Db      20 GINFLWGC 28

RESULT 8
US-11-096-568A-19834
; Sequence 19834, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19834
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(268)
; OTHER INFORMATION: Ceres Seq. ID no. 12374913
US-11-096-568A-19834

Query Match      56.2%; Score 40.5; DB 11; Length 268;
Best Local Similarity 54.5%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
Db      189 CGVWALLWGC 199

RESULT 9
US-10-374-954-23

Query Match      56.2%; Score 40.5; DB 9; Length 1998;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
Db      938 CGEWIETMWDC 948

RESULT 11
US-10-374-954-2
; Sequence 2, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-23

Query Match      56.2%; Score 40.5; DB 9; Length 1981;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
Db      921 CGEWIETMWDC 931

RESULT 10
US-10-374-954-21
; Sequence 21, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-21

Query Match      56.2%; Score 40.5; DB 9; Length 1998;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 CGYWL-TIWGC 10
Db      938 CGEWIETMWDC 948

RESULT 11
US-10-374-954-2
; Sequence 2, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
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; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-2

Query Match 56.2%; Score 40.5; DB 9; Length 2009;

Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10

Db 949 CGEWETWDC 959

RESULT 12

US-11-129-741-3641

; Sequence 3641, Application US/11129741

; Publication No. US20060034853A1

; GENERAL INFORMATION:

; APPLICANT: YUEN, KWOK YUNG

; APPLICANT: WOO, CHIU YAT PATRICK

; APPLICANT: LAU, KAR PUI SUSANNA

; APPLICANT: CHAN, KWOK HUNG

; APPLICANT: POON, LIT MAN

; APPLICANT: PEIRIS, JOSEPH S.M.

; APPLICANT: GUAN, YI

; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT

; FILE REFERENCE: V0690.0044

; CURRENT APPLICATION NUMBER: US/11/129,741

; CURRENT FILING DATE: 2005-05-16

; PRIOR APPLICATION NUMBER: 10/895,064

; PRIOR FILING DATE: 2004-07-21

; NUMBER OF SEQ ID NOS: 4257

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 3641

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Corononavirus-HKU1

US-11-129-741-3641

Query Match 55.6%; Score 40; DB 11; Length 10;

Best Local Similarity 71.4%; Pred. No. 8;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8

Db 2 GYWLCLW 8

RESULT 13

US-11-250-411-97

; Sequence 97, Application US/11250411

; Publication No. US20060034838A1

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: ITO, MIKITO

; APPLICANT: HANAI, NOBUO

; APPLICANT: KAWADA, YOKO

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: SHIBUYA, MASABUMI

; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY

; FILE REFERENCE: 249-107

; CURRENT APPLICATION NUMBER: US/11/250,411

; CURRENT FILING DATE: 2005-10-17

; PRIOR APPLICATION NUMBER: US/09/453,718

; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-97

Query Match 55.6%; Score 40; DB 11; Length 119;

Best Local Similarity 62.5%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9

Db 103 GYWFAYWG 110

RESULT 14

US-11-250-411-101

; Sequence 101, Application US/11250411

; Publication No. US20060034838A1

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: ITO, MIKITO

; APPLICANT: HANAI, NOBUO

; APPLICANT: KAWADA, YOKO

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: SHIBUYA, MASABUMI

; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY

; FILE REFERENCE: 249-107

; CURRENT APPLICATION NUMBER: US/11/250,411

; CURRENT FILING DATE: 2005-10-17

; PRIOR APPLICATION NUMBER: US/09/453,718

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: 09/315,051

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/119,014

; PRIOR FILING DATE: 1998-07-20

; PRIOR APPLICATION NUMBER: PCT/JP97/04259

; PRIOR FILING DATE: 1997-11-21

; NUMBER OF SEQ ID NOS: 111

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 101

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein

US-11-250-411-101

Query Match 55.6%; Score 40; DB 11; Length 119;

Best Local Similarity 62.5%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9

Db 103 GYWFAYWG 110

RESULT 15

US-11-250-411-86

; Sequence 86, Application US/11250411

; Publication No. US20060034838A1

; GENERAL INFORMATION:

us-10-046-922-35.rapbn

Tue May 2 12:32:40 2006

```

; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-86

```

```

Query Match      55.6%; Score 40; DB 11; Length 138;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      2 GYWLITWG 9
Db      122 GYWFAYWG 129

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Search completed: May 2, 2006, 09:33:44
Job time : 14.186 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 78.9535 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-67

Perfect score: 35

Sequence: 1 GYXXXXW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	97.1	10	4 AAB99759	Aab99759 Rhesus D
2	34	97.1	12	4 AAB99769	Aab99769 Rhesus D
3	34	97.1	452	4 AAU03644	Aau03644 Group B S
4	34	97.1	466	6 ABU21589	Abu21589 Protein e
5	34	97.1	469	8 ADS44861	Ads44861 Bacterial
6	34	97.1	472	6 ABU38334	Abu38334 Protein e
7	34	97.1	474	6 ABU24881	Abu24881 Protein e
8	34	97.1	475	5 ABP30560	Abp30560 Streptoco
9	34	97.1	475	6 ABU40245	Abu40245 Protein e
10	34	97.1	475	6 ABU29756	Abu29756 Protein e
11	34	97.1	475	8 ADS24700	Ads24700 Bacterial
12	34	97.1	475	8 ADV87906	Adv87906 Streptoco
13	34	97.1	475	8 ADV81356	Adv81356 Streptoco
14	34	97.1	475	8 ADV79159	Adv79159 Streptoco
15	34	97.1	478	7 ADC97241	Adc97241 E. faeciu
16	34	97.1	479	5 ABP26968	Abp26968 Streptoco
17	34	97.1	490	5 ABB55389	Abb55389 Lactococc
18	34	97.1	496	5 ABB55385	Abb55385 Lactococc
19	34	97.1	499	7 ABO74582	Abu74582 Pseudomon
20	34	97.1	506	6 ABU22414	Abu22414 Protein e
21	34	97.1	585	7 AUA49403	Aua49403 Multi-epi
22	34	97.1	585	8 AD024081	Ad024081 Epigene c
23	34	97.1	585	9 AD240583	Ad240583 HIV-TC mu
24	34	97.1	865	7 ABO70593	Abu70593 Pseudomon

25	33	94.3	10	5 ABP53931	Abp53931 VEGFR-3 b
26	33	94.3	10	5 ABP53932	Abp53932 VEGFR-3 b
27	33	94.3	69	4 AAO13595	Aao13595 Human pol
28	33	94.3	116	2 AAR15437	Aar15437 Heavy cha
29	33	94.3	116	6 ABO27261	Abu27261 ICAM-1 bi
30	33	94.3	116	6 ABO27269	Abu27269 ICAM-1 bi
31	33	94.3	116	6 ABO27263	Abu27263 ICAM-1 bi
32	33	94.3	116	6 ABO27259	Abu27259 ICAM-1 bi
33	33	94.3	116	6 ABO27255	Abu27255 ICAM-1 bi
34	33	94.3	116	6 ABO27277	Abu27277 Humanised
35	33	94.3	116	6 ABO27273	Abu27273 Murine IA
36	33	94.3	116	6 ABO27257	Abu27257 ICAM-1 bi
37	33	94.3	116	6 ABO27271	Abu27271 ICAM-1 bi
38	33	94.3	116	6 ABO27267	Abu27267 ICAM-1 bi
39	33	94.3	117	6 ABO27265	Abu27265 ICAM-1 bi
40	33	94.3	118	7 ADJ95639	Adj95639 Insulin-1
41	33	94.3	118	9 ADZ08201	Adz08201 IGF-speci
42	33	94.3	118	9 ADZ08173	Adz08173 IGF-speci
43	33	94.3	118	9 ADZ08158	Adz08158 IGF-speci
44	33	94.3	118	9 ADZ58532	Adz58532 VEGF rece
45	33	94.3	119	8 ADL11890	Adl11890 CDR trans

ALIGNMENTS

RESULT 1
AAB99759
ID AAB99759 standard; peptide; 10 AA.
XX
AC AAB99759;
XX
DT 21-SEP-2001 (first entry)
XX
DE Rhesus D antibody binding peptide SEQ ID NO:4.
XX
KW Rhesus D antibody binding peptide; Rhesus D; Rhd; identification;
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP;
KW idiopathic thrombocytopenic purpura; immunoglobulin.
XX
OS Homo sapiens.
XX
FN EP1106625-A1.
XX
PD 13-JUN-2001.
XX
PF 17-NOV-1999; 99EP-00122858.
XX
PR 17-NOV-1999; 99EP-00122858.
XX
PA (ZLBB-) ZLB BIOPLASMA AG.
XX
PI Miescher S, Hofmann A, Fisch I;
XX
WP1; 2001-393568/41.

Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the newborn (HDN).
Claim 1; Page 12; 19pp; English.

The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (i); (2) a vector (III) comprising one or more (ii) operably linked to an expression control system; (3) a cell (IV) comprising (ii) or (iii); (4) preparing (i); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid
 CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
 CC with foreign erythrocytes thereby avoiding the risk of transmission of
 CC viral diseases like AIDS and hepatitis B
 CC
 XX
 XX Sequence 10 AA;

Query Match 97.1%; Score 34; DB 4; Length 10;
 Best Local Similarity 57.1%; Pred. No. 12;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
 ||| |
 Db 1 GYWSAKW 7

RESULT 2
 AAB99769
 ID AAB99769 standard; peptide; 12 AA.

AC AAB99769;
 DT 21-SEP-2001 (first entry)

XX Rhesus D antibody related peptide #5.

DE Rhesus D antibody binding peptide; Rhesus D; RhD; identification;
 KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
 KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;
 KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.

XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..12

XX EP1106625-A1.

XX 13-JUN-2001.

XX 17-NOV-1999; 99BP-00122858.

XX 17-NOV-1999; 99BP-00122858.

XX (ZLBB-) ZLB BIOPLASMA AG.

XX Miescher S, Hofmann A, Fisch I;

XX WPI; 2001-383568/41.

XX Novel peptides capable of binding Rhesus D antibodies are used to
 PT manufacture an agent for the diagnosis, therapy or prophylaxis of
 PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the
 PT newborn (HDN).

XX Example 1; Page 8; 19pp; English.

XX The present invention describes peptides capable of binding Rhesus D
 CC antibodies (I). Also described in the present invention are: (1) a
 CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more
 CC (II) operably linked to an expression control system; (3) a cell (IV)
 CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)
 CC peptides having immunologic properties of Rhesus D protein epitopes
 CC comprising subjecting an antibody/antibody fragment recognising an
 CC epitope of Rhesus D protein to several panning rounds with a phage

CC display library, and identifying immunogenic peptide sequences which are
 CC mimotopes which differ in their amino acid sequence from the amino acid
 CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
 CC with foreign erythrocytes thereby avoiding the risk of transmission of
 CC viral diseases like AIDS and hepatitis B. The present sequence represents
 CC an anti-Rhesus D (RHD) antibody related peptide which is used in an
 CC example from the present invention
 XX
 XX Sequence 12 AA;

Query Match 97.1%; Score 34; DB 4; Length 12;
 Best Local Similarity 57.1%; Pred. No. 14;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXW 7
 ||| |
 Db 2 GYWSAKW 8

RESULT 3
 AAU03644
 ID AAU03644 standard; protein; 452 AA.

AC AAU03644;

XX 12-SEP-2001 (first entry)

XX Group B Streptococcus antigenic protein, ID-119.

XX Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;
 KW meningitis; neonate; antigenic; vaccine; infection; genital tract;
 KW capsid polysaccharide vaccination.

XX Streptococcus agalactiae.

XX WO200132882-A2.

XX 10-MAY-2001.

XX 07-SEP-2000; 2000WO-GB003437.

XX 07-SEP-1999; 99GB-00021125.

XX (MICR-) MICROBIAL TECHNIQS LTD.

XX Le Page RWF, Wells JM, Hanniffy SB;

XX WPI; 2001-316444/33.

XX N-PSDB; AAS07061.

XX New polypeptides derived from Streptococcus agalactiae are useful to
 PT provide detection of, and vaccination against, Group B Streptococcus
 PT infections, particularly to prevent infection in neonates.

XX Claim 1; Fig 1; 178pp; English.

XX AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus
 CC agalactiae) amino acid sequences of the invention. S. agalactiae is an
 CC encapsulated bacterium which is a major pathogen of humans causing sepsis
 CC and meningitis in neonates as well as adults. The S. agalactiae antigenic
 CC polypeptides are used to vaccinate against Group B Streptococcus
 CC infections, particularly to prevent infection in new born children
 CC arising from the maternal genital tract. An immunogenic composition is
 CC useful in the preparation of a medicament for the treatment or
 CC prophylaxis of Group B Streptococcus infection. The invention does not
 CC have the disadvantages of varied response rate associated with prior art

CC capsid polysaccharide vaccination against Group B Streptococcus
XX
SQ Sequence 452 AA;

Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 92 GYWSAW 98

RESULT 4
ABU21589
ID ABU21589 standard; protein; 466 AA.
XX
AC ABU21589;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #7116.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Burkholderia fungorum.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
WPI; 2003-029926/02.
DR N-PSDB; ACA25459.
XX
New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
Claim 25; SEQ ID NO 49513; 1766pp; English.
XX
The invention relates to an isolated nucleic acid comprising any one of
PS the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 466 AA;

Query Match 97.1%; Score 34; DB 6; Length 466;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 86 GYWSAW 92

RESULT 5
ADS44861
ID ADS44861 standard; protein; 469 AA.
XX
AC ADS44861;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #23291.
XX
Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
Bacteria.
OS
XX
US2003233675-A1.
XX
18-DEC-2003.
XX
20-FEB-2003; 2003US-00369493.
XX
21-FEB-2002; 2002US-0360039P.
XX
(CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
Claim 1; SEQ ID NO 23291; 122pp; English.
XX
The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 469 AA;

Query Match 97.1%; Score 34; DB 8; Length 469;

Best Local Similarity 57.1%; Pred. No. 4.6e+02; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 0;

QY 1 GYVXXXW 7

DB 97 GYVVASW 103

RESULT 6

ABU38334
ID ABU38334 standard; protein; 472 AA.

XX AC ABU38334;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #23861.

XX DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX KW Pseudomonas aeruginosa.

XX OS WO200277183-A2.

XX PN 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PF Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA42204.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 66258; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC on a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 472 AA;

Query Match 97.1%; Score 34; DB 6; Length 472;

Best Local Similarity 57.1%; Pred. No. 4.6e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVXXXW 7

DB 94 GYVISA W 100

RESULT 7

ABU24881
ID ABU24881 standard; protein; 474 AA.

XX AC ABU24881;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #10408.

XX DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX KW Clostridium botulinum.

XX OS WO200277183-A2.

XX PN 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PF Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA28751.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 52805; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC on a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 474 AA;
Query Match 97.1%; Score 34; DB 6; Length 474;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXW 7
DB 95 GYWLSAW 101
RESULT 8
ABP30560
ID ABP30560 standard; protein; 475 AA.
XX
AC ABP30560;
XX
DT 02-JUL-2002 (first entry)
XX Streptococcus polypeptide SEQ ID NO 10296.
DE Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX Streptococcus agalactiae.
OS Streptococcus agalactiae.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB004789.
XX
FF 27-OCT-2000; 2000GB-00026333.
PR

PR 24-NOV-2000; 2000GB-00028727.
PR 07-MAR-2001; 2001GB-00005640.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;
PI Tettelin H;
XX
XX WPI; 2002-352536/38.
DR N-PSDB; ABN71191.
XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
PS Claim 1; Page 4161; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 475 AA;
Query Match 97.1%; Score 34; DB 5; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXW 7
DB 92 GYWLSAW 98
RESULT 9
ABU40245
ID ABU40245 standard; protein; 475 AA.
XX
AC ABU40245;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by prokaryotic essential gene #25772.
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Pseudomonas putida.
OS Pseudomonas putida.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX

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PA (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA44115.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 68169; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 475 AA;
XX Query Match 97.1%; Score 34; DB 6; Length 475;
XX Best Local Similarity 57.1%; Pred. No. 4.6e+02;
XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 GYWXW 7
XX DB 93 GYWSAW 99
XX RESULT 10
XX ABU29756
XX ID ABU29756 standard; protein; 475 AA.
XX AC ABU29756;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #15283.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Enterococcus faecium.
XX PN WO200277183-A2.
XX
```

```
PD 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923F.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX N-PSDB; ACA33626.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 57680; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 475 AA;
XX Query Match 97.1%; Score 34; DB 6; Length 475;
XX Best Local Similarity 57.1%; Pred. No. 4.6e+02;
XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 GYWXW 7
XX DB 95 GYWSAW 101
XX RESULT 11
XX ADS24700
XX ID ADS24700 standard; protein; 475 AA.
XX AC ADS24700;
XX
```

DT 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #13733.
 DE Recombinant DNA construct; transformed plant; improved plant property;
 XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 XX bacterial polypeptide.
 XX Bacteria.
 OS US2003233675-A1.
 PN 18-DEC-2003.
 PD 20-FEB-2003; 2003US-00369493.
 PF 21-FEB-2002; 2002US-0360039P.
 PR (CAOY/) CAO Y.
 XX (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI WPI; 2004-061375/06.
 DR New recombinant DNA construct comprising a promoter positioned to provide
 XX for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 PT Claim 1; SEQ ID NO 13733; 122pp; English.
 PS The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX Sequence 475 AA;
 SQ Query Match 97.1%; Score 34; DB 8; Length 475;
 Best Local Similarity 57.1%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 GYXXXXX 7
 DB 93 GYWISAW 99

DT 24-FEB-2005 (first entry)
 XX Streptococcus agalactiae protein sequence, SEQ ID 300.
 DE Antibacterial; Vaccine; bacterial infection.
 KW Streptococcus agalactiae.
 OS FR2824074-A1.
 PN 31-OCT-2002.
 PD 26-APR-2001; 2001FR-00005642.
 PF 26-APR-2001; 2001FR-00005642.
 PR (INSP) INST PASTEUR.
 XX (CNRS) CNRS CENT NAT RECH SCI.
 PA Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
 PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu CP, Kunst F;
 PI WPI; 2004-101891/11.
 DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
 XX agalactiae for the development of vaccines, diagnostic tools, DNA chips
 PT and identification of therapeutic targets.
 PT Claim 6; SEQ ID NO 300; 2687pp; French.
 PS The present invention relates to novel Streptococcus agalactiae
 CC nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II;
 CC ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
 CC agalactiae involved in the synthesis of amino acids, cell membranes,
 CC intermediate (central) metabolism, energetic metabolism, fatty acid and
 CC phospholipid metabolism, nucleotide metabolism including purines,
 CC pyrimidines and/or nucleosides, regulatory functions, replication,
 CC transcription, translation, protein transport, adaptation to atypical
 CC conditions, sensitivity to medicines and/or analogues, functions related
 CC to transporters, biosynthesis of cofactors, prosthetic groups and
 CC transporters, cell membrane proteins and cellular machinery. (I) are
 CC useful for the detection and/or amplification of nucleic acids.
 CC Pharmaceutical composition comprising (I) or (II) are useful for
 CC treatment of a bacterial S. agalactiae infection. Note: W0200292818A2 is
 CC equivalent for the present basic patent FR2824074A1. W0200292818A2
 CC contains 6617 sequence whereas the present patent only contains 2344
 CC sequences.
 XX Sequence 475 AA;
 SQ Query Match 97.1%; Score 34; DB 8; Length 475;
 Best Local Similarity 57.1%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 GYXXXXX 7
 DB 92 GYWSAW 98

DT 24-FEB-2005 (first entry)
 XX ADV81356 standard; protein; 475 AA.
 AC ADV81356;
 XX ADV81356;
 XX 24-FEB-2005 (first entry)

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XX DE Streptococcus agalactiae protein, SEQ ID 2497.
XX KW Antibacterial; vaccine; bacterial infection.
XX KW Streptococcus agalactiae.
XX OS WO200292818-A2.
XX PN 21-NOV-2002.
XX PD 26-APR-2002; 2002WO-IB003059.
XX PF 26-APR-2001; 2001FR-00005642.
XX PR (INSP ) INST PASTEUR.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
XX PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P, Kunst F;
XX PI WPI; 2004-101891/11.
XX DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX PT agalactiae for the development of vaccines, diagnostic tools, DNA chips
XX PT and identification of therapeutic targets.
XX PS Claim 6; SEQ ID NO 2497; 439pp; French.
XX CC The present invention relates to novel Streptococcus agalactiae
XX CC nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
XX CC novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
XX CC nucleotide sequences encode polypeptides of S. agalactiae involved in the
XX CC synthesis of amino acids, cell membranes, intermediate (central)
XX CC metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
XX CC nucleotide metabolism including purines, pyrimidines and/or nucleosides,
XX CC regulatory functions, replication, transcription, translation, protein
XX CC transport, adaptation to atypical conditions, sensitivity to medicines
XX CC and/or analogues, functions related to transposons, biosynthesis of
XX CC cofactors, prosthetic groups and transporters, cell membrane proteins and
XX CC cellular machinery. (I) are useful for the detection and/or amplification
XX CC of nucleic acids. Pharmaceutical composition comprising (I) or (II) are
XX CC useful for treatment of a bacterial S. agalactiae infection. The complete
XX CC genome of Streptococcus agalactiae is given in ADV81204. Note: The
XX CC present patent is an equivalent for the basic patent FR2824074A1, which
XX CC contains only 2344 sequences.
XX SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVXXW 7
    ||| |
DB 92 GYVLSAW 98

RESULT 14
ADV79159
ID ADV79159 standard; protein; 475 AA.
XX AC * ADV79159;
XX DT 24-FEB-2005 (first entry)
XX DE Streptococcus agalactiae protein, SEQ ID 300.
XX KW Antibacterial; vaccine; bacterial infection.
XX OS Streptococcus agalactiae.
XX PN WO200292818-A2.

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVXXW 7
    ||| |
DB 92 GYVLSAW 98

RESULT 15
ADC97241
ID ADC97241 standard; protein; 478 AA.
XX AC ADC97241;
XX DT 01-JAN-2004 (first entry)
XX DE E. faecium protein sequence SEQ ID 6868.
XX KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
XX KW abdominal-pelvic infection.
XX OS Enterococcus faecium.
XX PN US6583275-B1.
XX PD 24-JUN-2003.
XX PF 30-JUN-1998; 98US-00107532.
XX PR 02-JUL-1997; 97US-0051571P.
XX PR 14-MAY-1998; 98US-0085598P.

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Tue May 2 12:32:41 2006

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XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA
XX PI Doucette-Stamm LA, Bush D;
XX XX
XX WPI; 2003-799836/75.
XX DR 'N-PSDB; ADC93587.
XX PT
XX PT New isolated nucleic acid derived from Enterococcus faecium encoding an
XX PT Enterococcus faecium polypeptide useful for detection, prevention and
XX PT treatment of a pathological condition resulting from a bacterial
XX PT infection.
XX PS Example 1; SEQ ID NO 6868; 243pp; English.
XX CC The invention relates to an isolated nucleic acid derived from
XX CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
XX CC one of 10 fully defined sequences given in the (or comprising 40
XX CC sequential nucleotides chosen from any of the nucleic acids, its
XX CC complement or sequences hybridising to it). Also included are a
XX CC recombinant vector comprising the nucleic acid operably linked to
XX CC transcription regulatory element, a cell comprising the vector and a
XX CC single-stranded probe comprising the nucleic acid. The nucleic acids are
XX CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
XX CC The nucleic acids is useful for diagnosing pathological conditions
XX CC resulting from E. faecium bacterial infection (e.g. urinary tract
XX CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
XX CC infection) and for screening drugs such as agonists and antagonists. The
XX CC nucleic acid is useful for recombinant production of Candida albicans -
XX CC derived peptides or antisense polypeptides. Pharmaceutical compositions
XX CC and vaccines containing the nucleic acid are useful for preventing or
XX CC treating Enterococcus faecium infections. The present sequence represents
XX CC one if the disclosed E. faecium proteins.
XX SQ Sequence 478 AA;
XX Query Match 97.1%; Score 34; DB 7; Length 478;
XX Best Local Similarity 57.1%; Pred. No. 4.7e+02;
XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GYXXXXXW 7
Db 98 GYWLSAW 104
Search completed: May 2, 2006, 08:54:55
Job time : 78.9535 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 12.6977 Seconds
(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-67
Perfect score: 35
Sequence: 1 GYWXSW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	72	T03190	hypothetical prote
2	34	97.1	108	S12193	hypothetical prote
3	34	97.1	345	T37139	hypothetical prote
4	34	97.1	469	D70048	ABC transporter (a
5	34	97.1	472	E83497	probable amino aci
6	34	97.1	475	T46745	arginine/ornithine
7	34	97.1	482	JH0110	arginine/ornithine
8	34	97.1	490	C86879	arginine/ornithine
9	34	97.1	497	G86878	IG heavy chain pre
10	33	94.3	142	C34903	CDPdiacylglycerol-
11	33	94.3	227	S73905	hypothetical prote
12	33	94.3	250	A69843	oligopeptide ABC t
13	33	94.3	289	G72215	hypothetical prote
14	33	94.3	360	A82047	probable transport
15	33	94.3	441	C95307	probable ABC trans
16	33	94.3	508	C95282	hypothetical prote
17	33	94.3	517	A13201	probable carbohydr
18	33	94.3	519	E83268	hypothetical prote
19	33	94.3	534	T15414	probable dipeptide
20	33	94.3	535	B95952	hypothetical prote
21	33	94.3	541	AC2392	hypothetical prote
22	33	94.3	563	AH2975	opha protein limpo
23	33	94.3	563	C98307	hypothetical prote
24	33	94.3	592	T15413	hypothetical prote
25	33	94.3	778	T31037	multidrug resistan
26	33	94.3	1502	T42216	lysis protein S -
27	32	91.4	71	S22505	hypothetical prote
28	32	91.4	83	E69903	hypothetical prote
29	32	91.4	187	G83047	hypothetical prote

hypothetical prote
hypothetical prote
probable mceF prot
aquaporin 8 - mous
aquaporin 8 - rat
phosphatidate cyti
phosphatidate cyti
protein F41H10.7 (I
hypothetical prote
siderophore/Surfac
conserved hypochet
probable secreted
oligopeptide trans
probable ABC trans
hypothetical prote

ALIGNMENTS

RESULT 1

T03190
hypothetical protein 72B - rice mitochondrion
C:Species: mitochondrion Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03190
R:Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Cell Physiol. 35, 1239-1244, 1994
A:Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existe
A:Reference number: Z14841; MUID:95211382; PMID:7545979
A:Accession: T03190
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <ITA>
A:Cross-references: UNIPROT:Q95302; UNIPARC:UPI000009746F; EMBL:D32052; NID:G769704; F
A:Experimental source: cultivar Nipponbare
A:Genetics:
A:Genome: mitochondrion
C:Keywords: mitochondrion

Query Match 97.1%; Score 34; DB 2; Length 72;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXSW 7
|||
Db 34 GYWXSW 40

RESULT 2

S12193
hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1
C:Species: Thiobacillus ferrooxidans
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S12193
R:Drolet, M.; Zanga, P.; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990
A:Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidan
A:Reference number: S12188; MUID:91125140; PMID:2280689
A:Accession: S12193
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <DRO>
A:Cross-references: UNIPROT:P20088; UNIPARC:UPI000013B9EC; EMBL:X52659; NID:G48158; P:
C:Genetics:
A:Genome: plasmid pTF1

Query Match 97.1%; Score 34; DB 2; Length 108;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXSW 7

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Db      89 GYWRSSW 95

RESULT 3
T37139
hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37139
R:Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21622
A:Accession: T37139
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <HAR>
A:Cross-references: UNIPROT:Q9S1R7; UNIPARC:UPI000000DB3A4; EMBL:AL109972; PIDN:CB53264.
A:Experimental source: strain A3(2)
C:Genetics:
C:Gene: SCOEDB:SCJ9A.03c
C:Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c

Query Match      97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      147 GYWAARW 153

RESULT 4
D70048
ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C:Accession: D70048
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Patro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70048
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-469 <KUN>
A:Cross-references: UNIPROT:O32204; UNIPARC:UPI0000060A54; GB:Z99121; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
C:Gene: yvsh
C:Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      97 GYWASW 103

RESULT 5
E83497
probable amino acid permease PAl194 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: E83497
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pat
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <STO>
A:Cross-references: UNIPROT:Q9I4B4; UNIPARC:UPI000000C529F; GB:AE004549; GB:AE004091; N
A:Experimental source: strain PAO1
C:Genetics:
C:Gene: PAl194
C:Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 472;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      94 GYWSAW 100

RESULT 6
T46745
arginine/ornithine antiporter [imported] - Lactobacillus sakei
C:Species: Lactobacillus sakei
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C:Accession: T46745
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez
J. Bacteriol. 180, 4154-4159, 1998
A:Title: Structural and functional analysis of the gene cluster encoding the enzymes o
A:Reference number: Z23141; MUID:98361904; PMID:9696763
A:Accession: T46745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <ZUN>
A:Cross-references: UNIPROT:O53092; UNIPARC:UPI0000125DAC; EMBL:AJ001330; NID:92764610
C:Genetics:
C:Gene: arcD
C:Function:
A:Description: necessary for arginine transport; involved in ornithine-arginine exchan
A:Pathway: arginine catabolism
C:Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 475;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      94 GYWSAW 100

RESULT 7
JH0110
arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004
C:Accession: JH0110; A82999
R:Luethi, B.; Baur, H.; Gamber, M.; Brunner, F.; Villevall, D.; Mercenier, A.; Haas, D.
Gene 87, 37-43, 1990
A:Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa co
A:Reference number: JH0110; MUID:90236296; PMID:2158926
A:Accession: JH0110

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A:Molecule type: DNA
A:Residues: 1-497 <STO>
A:Cross-references: UNIPROT:P09CE19; UNIPARC:UPI000006B95; GB:AE005176; PID:g12725079;
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: arcD2
C:Superfamily: ecotropic retrovirus receptor protein
Query Match 97.1%; Score 34; DB 2; Length 497;
Best Local Similarity 57.1%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXW 7
DB 93 GYWSAW 99
RESULT 10
C34903
IG heavy chain precursor V region (5-27) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C:Accession: C34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-r
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: C34903
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-142 <BED>
A:Cross-references: UNIPARC:UPI0000176C0F
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>
Query Match 94.3%; Score 33; DB 2; Length 142;
Best Local Similarity 57.1%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXW 7
DB 126 GYWFAYW 132
RESULT 11
S73905
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) p98A - M
N:Alternate names: hypothetical protein A65_orf227
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S73905
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73905
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-227 <HIM>
A:Cross-references: UNIPROT:P75520; UNIPARC:UPI000011886; EMBL:AE000057; GB:U00089; N
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Gene: pgsA
C:Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C:Keywords: transferase
Query Match 94.3%; Score 33; DB 2; Length 227;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXW 7

A:Molecule type: DNA
A:Residues: 1-482 <LUE>
A:Cross-references: UNIPROT:P18275; UNIPARC:UPI00000618AA; GB:M33223; NID:g151030; PIDN:
A:Experimental source: strain PA01
A:Note: the gene encoding this protein is located upstream of the arcABC genes which enc
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A82999
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-482 <STO>
A:Cross-references: UNIPARC:UPI00000618AA; GB:AE004930; GB:AE004091; NID:g9951472; PIDN:
A:Experimental source: strain PA01
C:Genetics:
A:Gene: arcD1
C:Superfamily: ecotropic retrovirus receptor protein
C:Keywords: transmembrane protein
Query Match 97.1%; Score 34; DB 2; Length 482;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXW 7
DB 94 GYWSAW 100
RESULT 8
C86879
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C:Accession: C86879
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <STO>
A:Cross-references: UNIPROT:P09CE15; UNIPARC:UPI000006B99; GB:AE005176; PID:g12725084; H
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: arcD1
C:Superfamily: ecotropic retrovirus receptor protein
Query Match 97.1%; Score 34; DB 2; Length 490;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXW 7
DB 93 GYWSAW 99
RESULT 9
G86878
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C:Accession: C86878
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86878
A:Status: preliminary
A:Molecule type: DNA

Db 84 GYWARXW 90
 |||
 RESULT 12
 A69843
 hypothetical protein yjba - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: A69843
 R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillette, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parto, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: A69843
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-250 <KUN>
 A:Cross-references: UNIPROT:O31597; UNIPARC:UPI0000060207; GB:Z99110; GB:AL009126; NID:9
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yjba
 C:Superfamily: Bacillus subtilis hypothetical protein yjba
 Query Match 94.3%; Score 33; DB 2; Length 250;
 Best Local Similarity 57.1%; Pred. No. 66;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GYWXW 7
 |||
 Db 185 GYWTW 191
 |||
 RESULT 13
 G72215
 oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: G72215
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: G72215
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-289 <ARN>
 A:Cross-references: UNIPROT:Q9X270; UNIPARC:UPI00000D385B; GB:AE001813; GB:AE000512; NID
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TWI748
 C:Superfamily: oligopeptide permease protein oppB
 Query Match 94.3%; Score 33; DB 2; Length 289;
 Best Local Similarity 57.1%; Pred. No. 75;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GYWXW 7
 |||

Db 11 GYWKAFW 17
 |||
 RESULT 14
 AE2047
 hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AE2047
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
 DNA Res. 8, 203-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2047
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-360 <KUR>
 A:Cross-references: UNIPROT:Q8YVP3; UNIPARC:UPI00000CE269; GB:BA000019; PIDN:BA073630.1
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all1931
 Query Match 94.3%; Score 33; DB 2; Length 360;
 Best Local Similarity 57.1%; Pred. No. 91;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GYWXW 7
 |||
 Db 127 GYWSGW 133
 |||
 RESULT 15
 CS5307
 probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) me
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 05-Oct-2004
 C:Accession: C95307
 R:Barnett, M.J.; Jones, R.F.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bov
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilic
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: C95307
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-441 <KUR>
 A:Cross-references: UNIPROT:Q92ZT6; UNIPARC:UPI00000CB08F; GB:AE006469; PIDN:AAK65021.1
 A:Experimental source: strain 1021, megaplasmid pSynA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
 hebaul, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, F
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma0684
 C:Superfamily: ecotropic retrovirus receptor protein
 Query Match 94.3%; Score 33; DB 2; Length 441;
 Best Local Similarity 57.1%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GYWXW 7
 |||
 Db 92 GYWSIW 98
 |||

us-10-046-922-67.rpr

Tue May 2 12:32:42 2006

Search completed: May 2, 2006, 08:56:19
Job time : 12.6977 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 79.2791 Seconds
(without alignments)

62.295 Million cell updates/sec

Title: US-10-046-922-67

Perfect score: 35

Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length:- 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, - and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	72	2	Q35302_ORYSA
2	34	97.1	108	1	YML2_THIFE
3	34	97.1	130	2	Q7U395_PROCHLORO
4	34	97.1	236	2	Q9XGW9_HUMAN IMMUN
5	34	97.1	253	2	Q32816_LACIC
6	34	97.1	294	2	Q8ET30_OCEIH
7	34	97.1	333	2	Q6F6U4_ACIAD
8	34	97.1	345	2	Q9S1R7_STRCO
9	34	97.1	451	2	Q6C74_BURMA
10	34	97.1	459	2	Q9KGV3_LACLA
11	34	97.1	464	2	Q84DL5_OENOE
12	34	97.1	465	2	Q613F7_BACAN
13	34	97.1	465	2	Q4MN56_BACCE
14	34	97.1	465	2	Q81HZ7_BACCR
15	34	97.1	465	2	Q63G16_BACCR
16	34	97.1	465	2	Q6HNI4_BACHK
17	34	97.1	465	2	Q73DL5_BACCI
18	34	97.1	465	2	Q81V71_BACAN
19	34	97.1	467	2	Q65F15_BACLD
20	34	97.1	469	2	Q6TK71_STRRT
21	34	97.1	469	2	Q32204_BACSU
22	34	97.1	471	2	Q6HP27_BACHK
23	34	97.1	471	2	Q73E85_BACCI
24	34	97.1	471	2	Q81IH9_BACCR
25	34	97.1	472	2	Q914E4_PSEAE
26	34	97.1	473	2	Q7NRJ8_CHRVO
27	34	97.1	475	1	ARCD_LACSK
28	34	97.1	475	2	Q4ZT00_PSESY
29	34	97.1	475	2	Q4KR76_PSEF5
30	34	97.1	475	2	Q4KR75_PSEF5
31	34	97.1	475	2	Q88P50_PSEPK

32	34	97.1	475	2	Q88P51_PSEPK	Q88P51 pseudomonas
33	34	97.1	475	2	Q8DWP9_STRAS	Q8DWP9 streptococc
34	34	97.1	475	2	Q8E2J7_STRAS	Q8E2J7 streptococc
35	34	97.1	478	1	ARCD_CLOPE	Q46170 clostridium
36	34	97.1	482	1	ARCD_PSEAE	P18275 pseudomonas
37	34	97.1	486	2	Q63U74_BURPS	O63U74 burkholderi
38	34	97.1	486	2	Q62KE0_BURMA	O62KE0 burkholderi
39	34	97.1	490	2	Q9CE15_LACLA	O9CE15 lactococcus
40	34	97.1	496	2	Q63L96_BURPS	Q63L96 burkholderi
41	34	97.1	497	2	Q9KGV0_LACLA	Q9KGV0 lactococcus
42	34	97.1	497	2	Q9CE19_LACLA	O9CE19 lactococcus
43	34	97.1	526	2	Q9K574_9LACT	O9K574 lactococcus
44	34	97.1	552	2	Q5LSW7_SILPO	O5LSW7 silicibacte
45	34	97.1	753	2	Q4TSN3_GSPHN	Q4TSN3 erythrobaet

ALIGNMENTS

RESULT 1
Q35302_ORYSA
ID Q35302_ORYSA PRELIMINARY; PRT; 72 AA.
AC Q35302
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-JAN-1998 (TREMUREL. 05, last sequence update)
DT 01-JUN-2003 (TREMUREL. 24, last annotation update)
DE ORF72B.
OS Oryza sativa (japonica cultivar-group).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,
RA Il'in I.V.;
RT "Structure of long and short copies of the mobile dispersed gene MDG3
of *Drosophila melanogaster*.";
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93308541; PubMed=7788722; DOI=10.1007/BF003113433;
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiura M.,
RA Hirai A.;
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is
transcribed from alternative promoters.";
RL Curr. Genet. 27:184-189(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95211382; PubMed=7545979;
RA Itadani H., Wakasugi T., Sugiura M., Nakazono M., Hirai A.;
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:
the existence of many sequences that correspond to parts of
mitochondrial genes in intergenic regions.";
RL Plant Cell Physiol. 35:1239-1244(1994).
DR -EMBL; D32052; BAA06811.1; -; Genomic_DNA.
DR PIR; T03190; T03190.
DR Gramene; Q35302; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 72 AA; 8155 MW; D42DE53BED28432E CRC64;

Query Match 97.1%; Score 34; DB 2; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYWXXXW 7
|||
Db 34 GYWSSHW 40

RESULT 2

```
YML2_THIFE
ID YML2_THIFE STANDARD; PRT; 108 AA.
AC P20088;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical 12.3 kDa protein in mobL 3' region (ORF 4).
OS Thiobacillus ferrooxidans.
CG Plasmid pTF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drole M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
RT ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC DR EMBL; X52699; CAA36930.1; -; Genomic_DNA.
CC DR PIR; S12193; S12193.
CC KW Hypothetical protein; Plasmid.
SQ SEQUENCE 108 AA; 12335 MW; AB667717C10A57E CRC64;

Query Match 97.1%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7
Db 89 GYRWSW 95

RESULT 3
Q7U395 PROMP PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible Adenoviral fiber protein (Repeat/shaf).
GN OrderedLocustNames=PW1067;
OS Prochlorococcus marinus subsp. pastoris (strain RCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572092; CAE19526.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; EE0F4A997FCA8CD8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 GYWXXW 7
Db 7 GYWTAW 13

RESULT 4
Q9GWG9_9HIV1 PRELIMINARY; PRT; 236 AA.
ID Q9GWG9_9HIV1 PRELIMINARY; PRT; 236 AA.
AC Q9GWG9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wzania A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.;
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
RT in perinatal human immunodeficiency virus (HIV) type 1 transmission:
RT the ariel project for the prevention of transmission of HIV from
RT mother to infant.";
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121641; AAD29013.1; -; Genomic_DNA.
DR HSP; P03366; IHRH.
DR SMR; Q9GWG9; 1-236.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR010659; RNaseH.
DR InterPro; IPR010661; RVT_thumb.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
DR PROSITE; PS00879; RNASE_H; 1.
KW Polyprotein.
FT NON_TER 1 236
FT SEQUENCE 236 AA; 27062 MW; 24D6BB0409A80B8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 236;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7
Db 129 GYQATW 135

RESULT 5
O32816 LACLC
ID O32816 LACLC PRELIMINARY; PRT; 253 AA.
AC O32816;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine/ornithine antiporter homolog ArcD (Fragment).
GN Name=arcD;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
```

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MG1363;
RX MEDLINE=97369814; PubMed=9226255;
RA Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
RT "Characterization of Lactococcus lactis UV-sensitive mutants obtained
by ISS1 transposition.";
RL J. Bacteriol. 179:4473-4479(1997).
DR EMBL; U81991; AAC45504.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
KW Transmembrane.
FT NON_TER 253
SQ SEQUENCE 253 AA; 26569 MW; 1CB8FAEF6C38FBB1 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 253;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 93 GYWSAW 99

RESULT 6
Q8ET30_OCEIH PRELIMINARY; PRT; 294 AA.
ID Q8ET30_OCEIH PRELIMINARY; PRT; 294 AA.
AC Q8ET30_OCEIH PRELIMINARY; PRT; 294 AA.
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ABC transporter permease.
GN OrderedLocusNames=OB0434;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC12390.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001526; ABC_3.
DR Pfam; PF00950; ABC-3; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;

Query Match 97.1%; Score 34; DB 2; Length 294;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 244 GYWIATW 250

RESULT 7
Q6F6U4_ACIAD PRELIMINARY; PRT; 333 AA.
ID Q6F6U4_ACIAD PRELIMINARY; PRT; 333 AA.

AC 06F6U4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative transporter; putative sodium/bile acid transporter family
protein.
GN OrderedLocusNames=ACIAD3583;
OS Acinetobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ADP1;
RX PubMed=15514110; DOI=10.1093/nar/gh910;
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Larrieu L., Cruveiller S., Robert C., Duprat S., Wincker P.,
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 32:5766-5779(2004).
DR EMBL; CR543861; CAG70223.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008508; F:bile acid:sodium symporter activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR002657; BilAc/Na_symport.
DR Pfam; PF01758; SBF; 1.
KW Complete proteome.
SQ SEQUENCE 333 AA; 36530 MW; 7C887F5127A40682 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 333;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 252 GYWSRW 258

RESULT 8
Q9S1R7_STRCO PRELIMINARY; PRT; 345 AA.
ID Q9S1R7_STRCO PRELIMINARY; PRT; 345 AA.
AC Q9S1R7_STRCO PRELIMINARY; PRT; 345 AA.
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein SC00224.
GN OrderedLocusNames=SC00224; ORFNames=SCU9A.03c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939104; CAB53264.1; -; Genomic_DNA.
DR PIR; T37139; T37139.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 345 AA; 36929 MW; 2364300993628588 CRC64;

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Query Match          97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 147 GYWAARW 153

RESULT 9
Q62C74_BURMA PRELIMINARY; PRT; 451 AA.
AC Q62C74;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Amino acid permease.
GN OrderedLocName=BMAA1038;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RC Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR ENBL; CP000011; AAU46467.1; -; Genomic_DNA.
DR TIGR; BMAA1038; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR Complete proteome.
SQ SEQUENCE 451 AA; 47344 MW; ED2DIADDEB0C4A55 CRC64;

Query Match          97.1%; Score 34; DB 2; Length 451;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 116 GYVWSAW 122

RESULT 10
Q9KGV3_LACIA PRELIMINARY; PRT; 459 AA.
AC Q9KGV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ArcD1.
GN Name=arcD1;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ML3;
RA Chou L., Weimer B., Xie Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

Query Match          97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 147 GYWAARW 153

RESULT 9
Q62C74_BURMA PRELIMINARY; PRT; 451 AA.
AC Q62C74;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Amino acid permease.
GN OrderedLocName=BMAA1038;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RC Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR ENBL; CP000011; AAU46467.1; -; Genomic_DNA.
DR TIGR; BMAA1038; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR Complete proteome.
SQ SEQUENCE 451 AA; 47344 MW; ED2DIADDEB0C4A55 CRC64;

Query Match          97.1%; Score 34; DB 2; Length 451;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 116 GYVWSAW 122

RESULT 10
Q9KGV3_LACIA PRELIMINARY; PRT; 459 AA.
AC Q9KGV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ArcD1.
GN Name=arcD1;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ML3;
RA Chou L., Weimer B., Xie Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

Query Match          97.1%; Score 34; DB 2; Length 464;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 94 GYWLSSW 100

RESULT 12
Q6I3F7_BACAN PRELIMINARY; PRT; 465 AA.
ID Q6I3F7;
AC Q6I3F7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	DB	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	Amino acid permease family protein.	DT	Amino acid permease family protein.
DE	OrderedLocusNames=BA050596;	DE	OrderedLocusNames=BA050596;
GN	Bacillus anthracis.	GN	Bacillus anthracis.
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;	OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC	Bacillus cereus group.	OC	Bacillus cereus group.
OX	NCBI_TaxID=1392;	OX	NCBI_TaxID=1392;
RN	[1]	RN	[1]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	Strain=Sterne;	RC	Strain=Sterne;
RA	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,	RA	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA	Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,	RA	Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA	Richardson P., Rubin E., Tice H.,	RA	Richardson P., Rubin E., Tice H.,
RT	"Complete genome sequence of Bacillus anthracis Sterne."	RT	"Complete genome sequence of Bacillus anthracis Sterne."
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.	RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF017225; AF52924.1; -; Genomic DNA.	DR	EMBL; AF017225; AF52924.1; -; Genomic DNA.
DR	GO; GO:0016021; C:integral to membrane; IEA.	DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.	DR	GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR	GO; GO:0006865; P:amino acid transport; IEA.	DR	GO; GO:0006865; P:amino acid transport; IEA.
DR	GO; GO:0006810; P:transport; IEA.	DR	GO; GO:0006810; P:transport; IEA.
DR	InterPro; IPR002293; AA/permease.	DR	InterPro; IPR002293; AA/permease.
DR	Pfam; PF00324; AA/permease; 1.	DR	Pfam; PF00324; AA/permease; 1.
KW	Transmembrane; Transport.	KW	Transmembrane; Transport.
SQ	SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;	SQ	SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;
QY	1 GYWXW 7	QY	1 GYWXW 7
DB	96 GYWAANW 102	DB	96 GYWAANW 102
RESULT 13		RESULT 13	
Q4MN56_BACCE		Q4MN56_BACCE	
ID	Q4MN56_BACCE PRELIMINARY; PRT; 465 AA.	ID	Q4MN56_BACCE PRELIMINARY; PRT; 465 AA.
AC	Q4MN56;	AC	Q4MN56;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)	DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)	DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE	Arginine/ornithine antiporter.	DE	Arginine/ornithine antiporter.
GN	Names=arcd; ORFNames=BCE_G9241_0606;	GN	Names=arcd; ORFNames=BCE_G9241_0606;
OS	Bacillus cereus G9241.	OS	Bacillus cereus G9241.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC	Bacillus cereus group.	OC	Bacillus cereus group.
OX	NCBI_TaxID=269801;	OX	NCBI_TaxID=269801;
RN	[1]	RN	[1]
RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RC	Strain=G9241;	RC	Strain=G9241;
RX	PubMed=15155910; DOI=10.1073/pnas.0402414101;	RX	PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA	Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,	RA	Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA	Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,	RA	Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA	Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,	RA	Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA	Ridstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,	RA	Ridstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA	Popovic T., Fraser C.M.,	RA	Popovic T., Fraser C.M.,
RT	"Identification of anthrax toxin genes in a Bacillus cereus associated	RT	"Identification of anthrax toxin genes in a Bacillus cereus associated
RL	with an illness resembling inhalation anthrax."	RL	with an illness resembling inhalation anthrax."
RL	Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).	RL	Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC	-1- CAUTION: The sequence shown here is derived from an	CC	-1- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is	CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.	CC	preliminary data.
DR	EMBL; AAEK0100024; EAL13575.1; -; Genomic DNA.	DR	EMBL; AAEK0100024; EAL13575.1; -; Genomic DNA.
SQ	SEQUENCE 465 AA; 50180 MW; F2A1540B055C90B9 CRC64;	SQ	SEQUENCE 465 AA; 50180 MW; F2A1540B055C90B9 CRC64;
QY	1 GYWXW 7	QY	1 GYWXW 7
DB	96 GYWAANW 102	DB	96 GYWAANW 102
RESULT 14		RESULT 14	
Q81H27_BACCR		Q81H27_BACCR	
ID	Q81H27_BACCR PRELIMINARY; PRT; 465 AA.	ID	Q81H27_BACCR PRELIMINARY; PRT; 465 AA.
AC	Q81H27;	AC	Q81H27;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Arginine/ornithine antiporter.	DE	Arginine/ornithine antiporter.
GN	OrderedLocusNames=BC06329;	GN	OrderedLocusNames=BC06329;
OS	Bacillus cereus (strain ATCC 14579 / DSM 31).	OS	Bacillus cereus (strain ATCC 14579 / DSM 31).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC	Bacillus cereus group.	OC	Bacillus cereus group.
OX	NCBI_TaxID=226900;	OX	NCBI_TaxID=226900;
RN	[1]	RN	[1]
RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;	RX	MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,	RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA	Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,	RA	Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA	Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,	RA	Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA	Greckhin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,	RA	Greckhin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA	Overbeek R., Kyrpides N.C.,	RA	Overbeek R., Kyrpides N.C.,
RT	"Genome sequence of Bacillus cereus and comparative analysis with	RT	"Genome sequence of Bacillus cereus and comparative analysis with
RT	Bacillus anthracis."	RT	Bacillus anthracis."
RL	Nature 423:87-91(2003).	RL	Nature 423:87-91(2003).
DR	EMBL; AE017000; AAP07646.1; -; Genomic DNA.	DR	EMBL; AE017000; AAP07646.1; -; Genomic DNA.
DR	GO; GO:0016020; C:membrane; IEA.	DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.	DR	GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR	GO; GO:0006865; P:amino acid transport; IEA.	DR	GO; GO:0006865; P:amino acid transport; IEA.
DR	GO; GO:0006810; P:transport; IEA.	DR	GO; GO:0006810; P:transport; IEA.
DR	InterPro; IPR004841; AA/permease.	DR	InterPro; IPR004841; AA/permease.
DR	Pfam; PF00324; AA/permease; 1.	DR	Pfam; PF00324; AA/permease; 1.
KW	Complete proteome.	KW	Complete proteome.
SQ	SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;	SQ	SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;
QY	1 GYWXW 7	QY	1 GYWXW 7
DB	96 GYWAANW 102	DB	96 GYWAANW 102
Query Match	97.1%; Score 34; DB 2; Length 465;	Query Match	97.1%; Score 34; DB 2; Length 465;
Best Local Similarity	57.1%; Pred. No. 6.8e+02;	Best Local Similarity	57.1%; Pred. No. 6.8e+02;
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT 15		RESULT 15	
Q63G16_BACCC		Q63G16_BACCC	
ID	Q63G16_BACCC PRELIMINARY; PRT; 465 AA.	ID	Q63G16_BACCC PRELIMINARY; PRT; 465 AA.
AC	Q63G16;	AC	Q63G16;
DT	25-OCT-2004 (TrEMBLrel. 28, Created)	DT	25-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE	Probable arginine/ornithine antiporter protein.	DE	Probable arginine/ornithine antiporter protein.
GN	Names=arcd;	GN	Names=arcd;
OS	Bacillus cereus (strain ZK).	OS	Bacillus cereus (strain ZK).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC	Bacillus cereus group.	OC	Bacillus cereus group.
OX	NCBI_TaxID=288681;	OX	NCBI_TaxID=288681;
RN	[1]	RN	[1]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,	RA	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA	Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,	RA	Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA	Richardson P., Rubin E., Tice H.,	RA	Richardson P., Rubin E., Tice H.,
RT	"Complete genome sequence of Bacillus cereus ZK."	RT	"Complete genome sequence of Bacillus cereus ZK."
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.	RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; CP000001; AAU19700.1; -; Genomic DNA.	DR	EMBL; CP000001; AAU19700.1; -; Genomic DNA.
DR	GO; GO:0016021; C:integral to membrane; IEA.	DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0016020; C:membrane; IEA.	DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.	DR	GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR	GO; GO:0006865; P:amino acid transport; IEA.	DR	GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/re1_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF0324; AA_permease; 1_region.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50178 MW; 55D7083AAE7B3958 CRC64;
Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. NO. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GIWXXXW 7
Db 96 GYWAANW 102

Search completed: May 2, 2006, 08:46:46
Job time : 79.2791 secs


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OM protein - protein search, using sw model

Run on:      May 2, 2006, 08:55:22 ; Search time 19.8605 Seconds
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Title:      US-10-046-922-67
Perfect score: 35
Sequence:    1 GYWXXW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2	34	97.1	499	2	US-09-252-991A-23328	Sequence 2328, A	
3	34	97.1	865	2	US-09-252-991A-19339	Sequence 19339, A	
4	33	94.3	543	2	US-09-252-991A-18597	Sequence 18597, A	
5	33	94.3	1498	2	US-09-792-616-9	Sequence 9, Appl	
6	33	94.3	1503	2	US-09-792-616-3	Sequence 3, Appl	
7	33	94.3	1503	2	US-09-647-140B-8	Sequence 8, Appl	
8	32	91.4	188	2	US-09-902-540-12675	Sequence 12675, A	
9	32	91.4	177	2	US-09-543-681A-7620	Sequence 7620, A	
10	32	91.4	252	2	US-09-502-653-10	Sequence 10, Appl	
11	32	91.4	263	2	US-09-610-906-12	Sequence 12, Appl	
12	32	91.4	274	2	US-09-248-796A-15791	Sequence 15791, A	
13	32	91.4	278	2	US-09-145-828A-11	Sequence 11, Appl	
14	32	91.4	278	2	US-09-903-456-18	Sequence 18, Appl	
15	32	91.4	278	2	US-09-621-670-17	Sequence 17, Appl	
16	32	91.4	339	2	US-09-252-991A-26841	Sequence 26841, A	
17	32	91.4	362	1	US-08-415-751-6	Sequence 6, Appl	
18	32	91.4	367	2	US-09-248-796A-15188	Sequence 15188, A	
19	32	91.4	492	2	US-09-107-532A-6945	Sequence 6945, A	
20	32	91.4	500	2	US-09-252-991A-21214	Sequence 21214, A	
21	31	88.6	185	2	US-10-808-807-12	Sequence 12, Appl	
22	31	88.6	342	2	US-09-252-991A-32031	Sequence 32031, A	
23	30	85.7	11	2	US-09-069-827A-87	Sequence 87, Appl	
24	30	85.7	16	2	US-09-620-091-81	Sequence 81, Appl	
25	30	85.7	519	2	US-09-198-452A-479	Sequence 479, A	
26	30	85.7	519	2	US-09-438-185A-454	Sequence 454, A	
27	30	85.7	554	2	US-09-252-991A-18441	Sequence 18441, A	

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Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
DB      98 GYLSAW 104

RESULT 2
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328

Query Match      97.1%; Score 34; DB 2; Length 499;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
DB      111 GYWSAW 117

RESULT 3
US-09-252-991A-19339
; Sequence 19339, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19339
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19339

Query Match      97.1%; Score 34; DB 2; Length 865;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
DB      487 GYWSAW 493

RESULT 4
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US-09-252-991A-18697
; Sequence 18697, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18697
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18697

Query Match      94.3%; Score 33; DB 2; Length 543;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
DB      331 GYWMVSW 337

RESULT 5
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match      94.3%; Score 33; DB 2; Length 1498;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
DB      960 GYWSLW 966

RESULT 6
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
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Tue May 2 12:32:41 2006

us-10-046-922-67.ra1

SEQ ID NO 3
 LENGTH: 1503
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-792-616-3

Query Match 94.3%; Score 33; DB 2; Length 1503;
 Best Local Similarity 57.1%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
 Db 965 GYWLW 971

RESULT 7
 US-09-647-140B-8
 ; Sequence 8, Application US/09647140B
 ; Patent No. 6803184
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox Chase Cancer Center
 ; APPLICANT: Krueh, Gary D.
 ; APPLICANT: Lee, Kun
 ; APPLICANT: Belinsky, Martin G.
 ; APPLICANT: Bain, Lisa J.
 ; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
 ; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
 ; FILE REFERENCE: FCCC 98-02
 ; CURRENT APPLICATION NUMBER: US/09/647,140B
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR FILING DATE: 1998-03-27
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 ; PRIOR FILING DATE: 1998-08-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0.
 ; SEQ ID NO 8
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 ; ORGANISM: Homo sapiens
 US-09-647-140B-8

Query Match 94.3%; Score 33; DB 2; Length 1503;
 Best Local Similarity 57.1%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
 Db 965 GYWLW 971

RESULT 8
 US-09-902-540-12675
 ; Sequence 12675, Application US/09902540
 ; Patent No. 683447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 12675
 ; LENGTH: 88
 ; TYPE: PRT
 ; ORGANISM: Myxococcus xanthus

US-09-902-540-12675

Query Match 91.4%; Score 32; DB 2; Length 88;
 Best Local Similarity 57.1%; Pred. No. 94;
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QY 1 GYXXXXXW 7
 Db 48 GYWLW 54

RESULT 9
 US-09-543-681A-7620
 ; Sequence 7620, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 7620
 ; LENGTH: 177
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-7620

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 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
 Db 43 GYWLW 49

RESULT 10
 US-09-502-653-10
 ; Sequence 10, Application US/09502653
 ; Patent No. 6331426
 ; GENERAL INFORMATION:
 ; APPLICANT: Bj rnvad, Mads Eskelund
 ; APPLICANT: Clausen, Ib Groth
 ; APPLICANT: Schleim, Martin
 ; APPLICANT: Bech, Lisbeth
 ; APPLICANT: stergaard, Peter Rahbek
 ; APPLICANT: Sj holm, Carsten
 ; TITLE OF INVENTION: NOVEL GALACTANASES
 ; FILE REFERENCE: 5481.200-US
 ; CURRENT APPLICATION NUMBER: US/09/502,653
 ; CURRENT FILING DATE: 2000-02-11
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 ; EARLIER FILING DATE: 1999-02-11
 ; EARLIER APPLICATION NUMBER: PA 1999 00799
 ; EARLIER FILING DATE: 1999-06-07
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 ; EARLIER FILING DATE: 1999-06-10
 ; NUMBER OF SEQ ID NOS: 52
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 ; SEQ ID NO 10
 ; LENGTH: 252
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 ; ORGANISM: Bacillus circulans
 US-09-502-653-10

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Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXW 7

Db 210 GYWEPAW 216

RESULT 11

US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkuth, Wayne
; APPLICANT: Klinger, Tod M.
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT
; FILE REFERENCE: PC-0012 CIP
; CURRENT APPLICATION NUMBER: US/09/610,906
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 09/226,994
; PRIOR FILING DATE: 1999-01-07
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; LENGTH: 263
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. 6566066: g2346968
; PUBLICATION INFORMATION:
US-09-610-906-12

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Best Local Similarity 57.1%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
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Db 224 GYWDHFW 230

RESULT 12

US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15791
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791

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Best Local Similarity 57.1%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 3;

Qy 1 GYWXXW 7

Db 84 GYWPITW 90

RESULT 13

US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
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; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

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Qy 1 GYWXXW 7

Db 108 GYWIFLW 114

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US-09-303-456-18
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; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
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; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-303-456-18

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Best Local Similarity 57.1%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 3;

Qy 1 GYWXXW 7

Db 108 GYWIFLW 114

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US-09-624-670-17
; Sequence 17, Application US/09624670

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; Patent No. 6913916
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P2
; CURRENT APPLICATION NUMBER: US/09/624,670
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-624-670-17

Query Match          91.4%; Score 32; DB 2; Length 278;
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Db      108 GYWIFLW 114

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GenCore version 5.1.7
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6	34	97.1	472	US-10-282-122A-66258	Sequence 66258, A
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11	34	97.1	506	US-10-282-122A-50338	Sequence 50338, A
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31	33	94.3	138	4	US-10-160-232-86	Sequence 86, Appl
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34	33	94.3	229	4	US-10-425-115-344695	Sequence 344695,
35	33	94.3	257	5	US-10-450-763-43035	Sequence 43035, A
36	33	94.3	296	4	US-10-156-781-9632	Sequence 9632, Ap
37	33	94.3	296	4	US-10-369-493-19811	Sequence 19811, A
38	33	94.3	466	4	US-10-369-493-16537	Sequence 16537, A
39	33	94.3	467	4	US-10-437-963-199114	Sequence 199114,
40	33	94.3	516	4	US-10-450-022-7	Sequence 7, Appl
41	33	94.3	526	4	US-10-450-022-4	Sequence 4, Appl
42	33	94.3	526	4	US-10-450-022-5	Sequence 5, Appl
43	33	94.3	526	5	US-10-450-185B-2	Sequence 2, Appl
44	33	94.3	526	5	US-10-450-185B-17	Sequence 17, Appl
45	33	94.3	526	5	US-10-433-747B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-425-115-308836
; Sequence 308836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 308836
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_44726C.1.pep
US-10-425-115-308836

Query Match 97.1%; Score 34; DB 4; Length 58;
Best Local Similarity 57.1%; Pred. NO. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVXXW 7
|||
Db 49 GYWGASW 55

RESULT 2
US-10-437-963-176036
; Sequence 176036, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

```

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176036
; LENGTH: 72
; TYPE: prt
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: clone ID
US-10-437-963-176036

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Query Match 97.1%; Score 34; DB 4; Length 72;
Best Local Similarity 57.1%;
Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels

Qy 1 GYWXXXW 7
db 34 GYWSSHW 40

RESULT 3

```

US-10-091-007-88
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial
; APPLICANT: Le Page, Richard W F
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88

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Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels

Qy 1 GYWXXXW 7
db 92 GYWLSAW 98

RESULT 4

```

US-10-282-122A-49513
/ Sequence 49513, Application US/10282122A
/ Publication No. US20040029129A1
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Wang, Liangsu
/
/ APPLICANT: Zamudio, Carlos
/
/ APPLICANT: Malone, Cheryl
/
/ APPLICANT: Haselbeck, Robert
/
/ APPLICANT: Ohlsen, Kari
/
/ APPLICANT: Zyskind, Judith
/
/ APPLICANT: Wall, Daniel
/
/ APPLICANT: Trawick, John
/
/ APPLICANT: Carr, Grant
/
/ APPLICANT: Yamamoto, Robert
/
/ APPLICANT: Forsyth, R.
/
/ APPLICANT: Xu, H.
/
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/
/ FILE REFERENCE: ELITRA.034A
/
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/
/ CURRENT FILING DATE: 2003-02-20
/
/ PRIOR APPLICATION NUMBER: 60/191,078
/
/ PRIOR FILING DATE: 2000-03-21
/
/ PRIOR APPLICATION NUMBER: 60/206,848

```

```

, PRIOR FILING DATE: 2000-05-23
, PRIOR APPLICATION NUMBER: 60/207,727
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: 60/230,335
, PRIOR FILING DATE: 2000-09-06
, PRIOR APPLICATION NUMBER: 60/230,347
, PRIOR FILING DATE: 2000-09-09
, PRIOR APPLICATION NUMBER: 60/242,578
, PRIOR FILING DATE: 2000-10-23
, PRIOR APPLICATION NUMBER: 60/253,625
, PRIOR FILING DATE: 2000-11-27
, PRIOR APPLICATION NUMBER: 60/257,931
, PRIOR FILING DATE: 2000-12-22
, PRIOR APPLICATION NUMBER: 60/267,636
, PRIOR FILING DATE: 2001-02-09
, PRIOR APPLICATION NUMBER: 60/269,308
, PRIOR FILING DATE: 2001-02-16
, Remaining Prior Application data removed
, NUMBER OF SEQ ID NOS: 78614
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 49513
, LENGTH: 466
, TYPE: PRT
, ORGANISM: Burkholderia fungorum
US-10-282-122A-49513

```

Query Match 97.1%; Score 34; DB 4; Length 466;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4: Conservative 0; Mismatches 3; Indels

Qy 1 GYXXXXXW 7
86 GYWVSAW 92

RESULT 5

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US-10-369-493-23291
; Sequence 23291, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBI-
; TITLE OF INVENTION: PLANTS WITH IMPROVED
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
; LENGTH: 469
; TYPE: prt
; ORGANISM: Bacillus subtilis
US-10-369-493-23291

```

```

Query Match      97.1%; Score 34; DB 4; Length 469;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4: Conservative 0; Mismatches 3; Indels

```

Qy 1 GYXXXXW 7
|||
97 GYXVASW 103

RESULT 6

US-10-282-122A-66258
; Sequence 66258, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

APPLICANT: Wang, Liangu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66258
LENGTH: 472
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66258
Query Match 97.1%; Score 34; DB 4; Length 472;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXW 7
Db 94 GYWISAW 100
RESULT 7
US-10-282-122A-52805
Sequence 52805, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52805
LENGTH: 474
TYPE: PRT
ORGANISM: Clostridium botulinum
US-10-282-122A-52805
Query Match 97.1%; Score 34; DB 4; Length 474;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXW 7
Db 95 GYWISAW 101
RESULT 8
US-10-369-493-13733
Sequence 13733, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13733
LENGTH: 475
TYPE: PRT
ORGANISM: Pseudomonas fluorescens
US-10-369-493-13733
Query Match 97.1%; Score 34; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXW 7
Db 93 GYWISAW 99

RESULT 9

US-10-282-122A-57680
; Sequence 57680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 57680

LENGTH: 475

TYPE: PRT

ORGANISM: Enterococcus faecium

US-10-282-122A-57680

Query Match 97.1%; Score 34; DB 4; Length 475;

Best Local Similarity 57.1%; Pred No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7

|||

DB 95 GYWLSAW 101

RESULT 10

US-10-282-122A-68169

; Sequence 68169, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 68169

LENGTH: 475

TYPE: PRT

ORGANISM: Pseudomonas putida

US-10-282-122A-68169

Query Match 97.1%; Score 34; DB 4; Length 475;

Best Local Similarity 57.1%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7

|||

DB 93 GYWISAW 99

RESULT 11

US-10-282-122A-50338

; Sequence 50338, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50338
LENGTH: 506
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50338

Query Match 97.1%; Score 34; DB 4; Length 506;
Best Local Similarity 57.1%; Pred. No. 7e+02; Indels 3; Mismatches 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GYXXXXX 7
Db 124 GYWISAW 130

RESULT 12
US-09-894-018-87
Sequence 87, Application US/09894018
Patent No. US20020119127A1
GENERAL INFORMATION:
APPLICANT: EPIMMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denise
APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
FILE REFERENCE: 39963-20033.00
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 87
LENGTH: 585
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV-TC
US-09-894-018-87

Query Match 97.1%; Score 34; DB 3; Length 585;
Best Local Similarity 57.1%; Pred. No. 7.9e+02; Indels 3; Mismatches 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GYXXXXX 7
Db 22 GYQWQATW 28

RESULT 13
US-10-474-960A-87
Sequence 87, Application US/10474960A
Publication No. US20040248113A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denise
APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
Acid Constructs and Peptides Encoded Thereby
FILE REFERENCE: 2060.0320004
CURRENT APPLICATION NUMBER: US/10/474,960A
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: PCT/US02/09877
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/894,018
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 87
LENGTH: 585
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV-TC
US-10-474-960A-87

Query Match 97.1%; Score 34; DB 5; Length 585;
Best Local Similarity 57.1%; Pred. No. 7.9e+02; Indels 3; Mismatches 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GYXXXXX 7
Db 22 GYQWQATW 28

RESULT 14
US-10-046-922-34
Sequence 34, Application US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 10
TYPE: PRT
ORGANISM: isolated peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
LOCATION: (10)..(10)
OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match 94.3%; Score 33; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 47; Indels 3; Mismatches 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GYXXXXX 7
Db 22 GYQWQATW 28

Db 2 GYWLTIW 8

RESULT 15
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match 94.3%; Score 33; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYXXXXW 7
Db 2 GYWLTIW 8

Search completed: May 2, 2006, 09:32:39
Job time : 65.1163 secs

GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17; Search time 9.93023 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-67

Perfect score: 35

Sequence: 1 GYXXXXX 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA_New.*
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3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	464	11	US-11-087-099-1003
2	34	97.1	469	11	US-11-087-099-11321
3	34	97.1	471	11	US-11-188-298-19864
4	34	97.1	472	11	US-11-087-099-12291
5	34	97.1	475	11	US-11-087-099-1870
6	34	97.1	475	11	US-11-087-099-2298
7	34	97.1	475	11	US-11-087-099-7571
8	34	97.1	475	11	US-11-188-298-6764
9	34	97.1	476	11	US-11-087-099-1256
10	34	97.1	478	11	US-11-087-099-7019
11	34	97.1	478	11	US-11-087-099-9555
12	34	97.1	478	11	US-11-188-298-8872
13	34	97.1	482	11	US-11-087-099-4146
14	34	97.1	491	11	US-11-087-099-9097
15	33	94.3	119	11	US-11-250-411-97
16	33	94.3	119	11	US-11-250-411-101
17	33	94.3	138	11	US-11-250-411-86
18	33	94.3	138	11	US-11-250-411-90
19	33	94.3	441	11	US-11-087-099-2305
20	33	94.3	456	11	US-11-087-099-8799
21	33	94.3	474	11	US-11-087-099-10672

22 94.3 1023 9 US-10-995-561-968 Sequence 968, App
23 91.4 122 9 US-10-467-657-5906 Sequence 5906, App
24 91.4 445 11 US-11-079-463-8428 Sequence 8428, App
25 91.4 480 11 US-11-079-463-7586 Sequence 7586, App
26 91.4 566 11 US-11-188-298-3470 Sequence 3470, App
27 91.4 986 11 US-11-079-463-10025 Sequence 10025, A
28 88.6 10 11 US-11-129-741-3641 Sequence 3641, App
29 85.7 16 9 US-10-923-988-81 Sequence 81, Appl
30 85.7 2335 9 US-10-821-234-1610 Sequence 1610, App
31 82.9 347 9 US-10-506-454-1117 Sequence 1117, App
32 82.9 400 9 US-10-467-657-7096 Sequence 7096, App
33 82.9 488 11 US-11-087-099-7125 Sequence 7125, App
34 80.0 8 11 US-11-045-024-4376 Sequence 4376, App
35 80.0 8 11 US-11-045-024-4377 Sequence 4377, App
36 80.0 8 11 US-11-045-024-12720 Sequence 12720, A
37 80.0 8 11 US-11-045-024-12755 Sequence 12755, A
38 80.0 9 11 US-11-045-024-262 Sequence 262, App
39 80.0 9 11 US-11-045-024-263 Sequence 263, App
40 80.0 9 11 US-11-045-024-4500 Sequence 4500, App
41 80.0 9 11 US-11-045-024-4501 Sequence 4501, App
42 80.0 9 11 US-11-045-024-6570 Sequence 6570, App
43 80.0 9 11 US-11-045-024-6641 Sequence 6641, App
44 80.0 10 11 US-11-045-024-2129 Sequence 2129, App
45 80.0 10 11 US-11-045-024-2130 Sequence 2130, App

ALIGNMENTS

RESULT 1
US-11-087-099-1003
; Sequence 1003, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1003
; LENGTH: 464
; TYPE: PRT
; ORGANISM: *Oenococcus oeni*
US-11-087-099-1003

Query Match 97.1%; Score 34; DB 11; Length 464;
Best Local Similarity 57.1%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7
DB 94 GYWLSSW 100

RESULT 2
US-11-087-099-11321
; Sequence 11321, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11321
; LENGTH: 469
; TYPE: PRT
; ORGANISM: *Bacillus subtilis* subsp. *subtilis* str. 168
US-11-087-099-11321

Query Match 97.1%; Score 34; DB 11; Length 469;

Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
1 GYXXXXX 7	97.1%	57.1%	34	11	3	0	0
97 GYVWASW 103	97.1%	57.1%	34	11	3	0	0
<p>US-11-188-298-19864</p> <p>Sequence 19864, Application US/11188298</p> <p>Publication No. US20060075522A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Abad, Mark S. et al.</p> <p>TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT</p> <p>FILE REFERENCE: 38-21(53452)B</p> <p>CURRENT APPLICATION NUMBER: US/11/188,298</p> <p>CURRENT FILING DATE: 2005-07-22</p> <p>PRIOR APPLICATION NUMBER: 60/592,978</p> <p>PRIOR FILING DATE: 2004-07-31</p> <p>NUMBER OF SEQ ID NOS: 22569</p> <p>SEQ ID NO 19864</p> <p>LENGTH: 471</p> <p>TYPE: PRT</p> <p>ORGANISM: Bacillus cereus ATCC 14579</p> <p>US-11-188-298-19864</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
1 GYXXXXX 7	97.1%	57.1%	34	11	3	0	0
92 GYVLSAW 98	97.1%	57.1%	34	11	3	0	0
<p>US-11-087-099-12291</p> <p>Sequence 12291, Application US/11087099</p> <p>Publication No. US20060041961A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Abad, Mark S. et al.</p> <p>TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT</p> <p>FILE REFERENCE: 38-21(53450)B EP</p> <p>CURRENT APPLICATION NUMBER: US/11/087,099</p> <p>CURRENT FILING DATE: 2005-03-22</p> <p>NUMBER OF SEQ ID NOS: 12464</p> <p>SEQ ID NO 12291</p> <p>LENGTH: 472</p> <p>TYPE: PRT</p> <p>ORGANISM: Pseudomonas aeruginosa PAO1</p> <p>US-11-087-099-12291</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
1 GYXXXXX 7	97.1%	57.1%	34	11	3	0	0
94 GYVLSAW 100	97.1%	57.1%	34	11	3	0	0
<p>US-11-087-099-1870</p> <p>Sequence 1870, Application US/11087099</p> <p>Publication No. US20060041961A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Abad, Mark S. et al.</p> <p>TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT</p> <p>FILE REFERENCE: 38-21(53450)B EP</p> <p>CURRENT APPLICATION NUMBER: US/11/087,099</p> <p>CURRENT FILING DATE: 2005-03-22</p> <p>NUMBER OF SEQ ID NOS: 12464</p> <p>SEQ ID NO 1870</p> <p>LENGTH: 475</p> <p>TYPE: PRT</p> <p>ORGANISM: Pseudomonas syringae pv. syringae B728a</p> <p>US-11-087-099-1870</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
1 GYXXXXX 7	97.1%	57.1%	34	11	3	0	0
93 GYVLSAW 99	97.1%	57.1%	34	11	3	0	0
<p>US-11-087-099-2298</p> <p>Sequence 2298, Application US/11087099</p> <p>Publication No. US20060041961A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Abad, Mark S. et al.</p> <p>TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT</p> <p>FILE REFERENCE: 38-21(53450)B EP</p> <p>CURRENT APPLICATION NUMBER: US/11/087,099</p> <p>CURRENT FILING DATE: 2005-03-22</p> <p>NUMBER OF SEQ ID NOS: 12464</p> <p>SEQ ID NO 2298</p> <p>LENGTH: 475</p> <p>TYPE: PRT</p> <p>ORGANISM: Pseudomonas putida KT2440</p> <p>US-11-087-099-2298</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
1 GYXXXXX 7	97.1%	57.1%	34	11	3	0	0
93 GYVLSAW 99	97.1%	57.1%	34	11	3	0	0
<p>US-11-087-099-7571</p> <p>Sequence 7571, Application US/11087099</p> <p>Publication No. US20060041961A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Abad, Mark S. et al.</p> <p>TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT</p> <p>FILE REFERENCE: 38-21(53450)B EP</p> <p>CURRENT APPLICATION NUMBER: US/11/087,099</p> <p>CURRENT FILING DATE: 2005-03-22</p> <p>NUMBER OF SEQ ID NOS: 12464</p> <p>SEQ ID NO 7571</p> <p>LENGTH: 475</p> <p>TYPE: PRT</p> <p>ORGANISM: Pseudomonas putida KT2440</p> <p>US-11-087-099-7571</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
1 GYXXXXX 7	97.1%	57.1%	34	11	3	0	0
93 GYVLSAW 99	97.1%	57.1%	34	11	3	0	0
<p>US-11-087-099-6764</p> <p>Sequence 6764, Application US/11188298</p> <p>Publication No. US20060075522A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Abad, Mark S. et al.</p> <p>TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT</p> <p>FILE REFERENCE: 38-21(53450)B EP</p> <p>CURRENT APPLICATION NUMBER: US/11/087,099</p> <p>CURRENT FILING DATE: 2005-03-22</p> <p>NUMBER OF SEQ ID NOS: 12464</p> <p>SEQ ID NO 6764</p> <p>LENGTH: 475</p> <p>TYPE: PRT</p> <p>ORGANISM: Pseudomonas syringae pv. syringae B728a</p> <p>US-11-087-099-6764</p>							

RESULT 9
US-11-087-099-1256
; Sequence 1256, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6764
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Lactobacillus sakei
US-11-188-298-6764

Query Match 97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
| | | | |
DB 94 GYWLSAW 100

RESULT 10
US-11-087-099-7019
; Sequence 7019, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7019
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-087-099-7019

Query Match 97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
| | | | |
DB 95 GYWLSAW 101

RESULT 11
US-11-087-099-9555
; Sequence 9555, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9555
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-087-099-9555

Query Match 97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
| | | | |
DB 98 GYWLSAW 104

RESULT 12
US-11-188-298-8872
; Sequence 8872, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8872
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-188-298-8872

Query Match 97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
| | | | |
DB 96 GYWLSAW 102

RESULT 13
US-11-087-099-4146
; Sequence 4146, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4146
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-087-099-4146

Query Match 97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
| | | | |
DB 96 GYWLSAW 102

RESULT 14
US-11-087-099-4146
; Sequence 4146, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4146
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-087-099-4146

Query Match 97.1%; Score 34; DB 11; Length 482;

Best Local Similarity 57.1%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 103 GYWFAYW 109
Search completed: May 2, 2006, 09:33:44
Job time: 9.93023 secs

QY 1 GYWXW 7
Db 94 GYWISAW 100

RESULT 14

US-11-087-099-9097
; Sequence 9097, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9097
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens Pfo-1
US-11-087-099-9097

Query Match 97.1%; Score 34; DB 11; Length 491;
Best Local Similarity 57.1%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 109 GYWISAW 115

RESULT 15

US-11-250-411-97
; Sequence 97, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-97

Query Match 94.3%; Score 33; DB 11; Length 119;
Best Local Similarity 57.1%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 109 GYWISAW 115

Tue May 2 12:32:42 2006

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.2326 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 35

Sequence: 1 GYVXXXWX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: Genesep21990s.*
- 3: Genesep22000s.*
- 4: Genesep22001s.*
- 5: Genesep22002s.*
- 6: Genesep22003as.*
- 7: Genesep22003bs.*
- 8: Genesep22004s.*
- 9: Genesep22005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	10	4 AAB99759	Aab99759 Rhesus D
2	34	97.1	12	4 AAB99769	Aab99769 Rhesus D
3	34	97.1	452	4 AAU03644	Aau03644 Group B S
4	34	97.1	466	6 ABU21589	Abu21589 Protein e
5	34	97.1	469	8 ADS44861	Ads44861 Bacterial
6	34	97.1	472	6 ABU38334	Abu38334 Protein e
7	34	97.1	474	6 ABU24881	Abp24881 Protein e
8	34	97.1	475	5 ABP30560	Abp30560 Streptoco
9	34	97.1	475	6 ABU40245	Abu40245 Protein e
10	34	97.1	475	6 ABU29756	Abu29756 Protein e
11	34	97.1	475	8 ADS24700	Ads24700 Bacterial
12	34	97.1	475	8 ADV87906	Adv87906 Streptoco
13	34	97.1	475	8 ADV81356	Adv81356 Streptoco
14	34	97.1	475	8 ADV79159	Adv79159 Streptoco
15	34	97.1	478	7 ADC97241	Adc97241 E. faeciu
16	34	97.1	479	5 ABP26968	Abp26968 Streptoco
17	34	97.1	490	5 ABB55389	Abb55389 Lactococc
18	34	97.1	496	5 ABB55385	Abb55385 Lactococc
19	34	97.1	499	7 ABO74582	Abu74582 Pseudomon
20	34	97.1	506	6 ABU22414	Abu22414 Protein e
21	34	97.1	585	7 ADA49403	Ada49403 Multi-epi
22	34	97.1	585	8 ADQ24081	Adq24081 Epigene c
23	34	97.1	585	9 ADZ40583	Adz40583 HIV-TC mu
24	34	97.1	865	7 ABO70593	Abu70593 Pseudomon

25	33	94.3	10	5 ABP53931	Abp53931 VEGFR-3 b
26	33	94.3	10	5 ABP53932	Abp53932 VEGFR-3 b
27	33	94.3	69	4 AAO13595	Aao13595 Human pol
28	33	94.3	116	2 AAR15437	Aar15437 Heavy cha
29	33	94.3	116	6 ABO27261	Abu27261 ICAM-1 b1
30	33	94.3	116	6 ABO27269	Abu27269 ICAM-1 b1
31	33	94.3	116	6 ABO27263	Abu27263 ICAM-1 b1
32	33	94.3	116	6 ABO27259	Abu27259 ICAM-1 b1
33	33	94.3	116	6 ABO27255	Abu27255 ICAM-1 b1
34	33	94.3	116	6 ABO27277	Abu27277 Humanised
35	33	94.3	116	6 ABO27273	Abu27273 Murine 1A
36	33	94.3	116	6 ABO27257	Abu27257 ICAM-1 b1
37	33	94.3	116	6 ABO27271	Abu27271 ICAM-1 b1
38	33	94.3	116	6 ABO27267	Abu27267 ICAM-1 b1
39	33	94.3	117	6 ABO27265	Abu27265 ICAM-1 b1
40	33	94.3	118	7 ADJ95639	Adj95639 Insulin-1
41	33	94.3	118	9 ADZ08201	Adz08201 IGF-speci
42	33	94.3	118	9 ADZ08173	Adz08173 IGF-speci
43	33	94.3	118	9 ADZ08158	Adz08158 IGF-speci
44	33	94.3	118	9 ADZ58532	Adz58532 VEGF rece
45	33	94.3	119	8 ADL11890	Adl11890 CDR trans

ALIGNMENTS

RESULT 1
AAB99759
ID AAB99759 standard; peptide; 10 AA.
XX
AC AAB99759;
XX
DT 21-SEP-2001 (first entry)
XX
DE Rhesus D antibody binding peptide SEQ ID NO:4.
XX
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP;
KW idiopathic thrombocytopenic purpura; immunoglobulin.
XX
OS Homo sapiens.
XX
PN EPL106625-AL.
XX
PD 13-JUN-2001.
XX
PF 17-NOV-1999; 99EP-00122858.
XX
PR 17-NOV-1999; 99EP-00122858.
XX
PA (ZLBB-) ZLB BIOPLASMA AG.
XX
PI Miescher S, Hofmann A, Fisch I;
XX
WR 2001-383568/41.

Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the newborn (HDN).
Claim 1; Page 12; 19pp; English.
The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (1); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (1); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid
 CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
 CC with foreign erythrocytes thereby avoiding the risk of transmission of
 CC viral diseases like AIDS and hepatitis B
 CC
 XX Sequence 10 AA;
 XX
 XX Query Match 97.1%; Score 34; DB 4; Length 10;
 XX Best Local Similarity 57.1%; Pred. No. 12;
 XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1 GYWXXXW 7
 ||| |
 Db 1 GYWSAKW 7
 ||| |
 RESULT 2
 AAB99769
 ID AAB99769 standard; peptide; 12 AA.
 XX
 AC AAB99769;
 XX
 DT 21-SEP-2001 (first entry)
 XX
 DE Rhesus D antibody related peptide #5.
 XX
 DE Rhesus D antibody binding peptide; Rhesus D; RhD; identification;
 KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
 KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;
 KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Disulfide-bond 1..12
 XX
 XX EP1106625-A1.
 XX
 XX 13-JUN-2001.
 XX
 XX 17-NOV-1999; 99EP-00122858.
 XX
 XX 17-NOV-1999; 99EP-00122858.
 XX
 XX (ZLBB-) ZLB BIOPLASMA AG.
 XX
 XX Miescher S, Hofmann A, Fisch I;
 PI
 XX WPI; 2001-383568/41.
 XX
 XX Novel peptides capable of binding Rhesus D antibodies are used to
 XX manufacture an agent for the diagnosis, therapy or prophylaxis of
 XX diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
 XX newborn (HDN).
 XX
 XX Example 1; Page 8; 19pp; English.
 XX
 CC The present invention describes peptides capable of binding Rhesus D
 CC antibodies (I). Also described in the present invention are: (1) a
 CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more
 CC (II) operably linked to an expression control system; (3) a cell (IV)
 CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)
 CC peptides having immunologic properties of Rhesus D protein epitopes
 CC comprising subjecting an antibody/antibody fragment recognising an
 CC epitope of Rhesus D protein to several panning rounds with a phase

CC display library, and identifying immunogenic peptide sequences which are
 CC mimotopes which differ in their amino acid sequence from the amino acid
 CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
 CC with foreign erythrocytes thereby avoiding the risk of transmission of
 CC viral diseases like AIDS and hepatitis B. The present sequence represents
 CC an anti-Rhesus D (RhD) antibody related peptide which is used in an
 CC example from the present invention
 XX
 XX Sequence 12 AA;
 XX
 XX Query Match 97.1%; Score 34; DB 4; Length 12;
 XX Best Local Similarity 57.1%; Pred. No. 14;
 XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1 GYWXXXW 7
 ||| |
 Db 2 GYWSAKW 8
 ||| |
 RESULT 3
 AAU03644
 ID AAU03644 standard; protein; 452 AA.
 XX
 AC AAU03644;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Group B Streptococcus antigenic protein, ID-119.
 XX
 DE Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;
 KW meningitis; neonate; antigenic; vaccine; infection; genital tract;
 KW capsid polysaccharide vaccination.
 XX
 XX Streptococcus agalactiae.
 XX
 XX WO200132882-A2.
 XX
 XX 10-MAY-2001.
 XX
 XX 07-SEP-2000; 2000WO-GB003437.
 XX
 XX 07-SEP-1999; 99GB-00021125.
 XX
 XX (MICR-) MICROBIAL TECHNIQS LTD.
 XX
 XX Le Page RWF, Wells JW, Hanniffy SB;
 PI
 XX WPI; 2001-316444/33.
 XX
 XX N-PSDB; AAS07061.
 XX
 XX New polypeptides derived from Streptococcus agalactiae are useful to
 XX provide detection of, and vaccination against, Group B Streptococcus
 XX infections, particularly to prevent infection in neonates.
 XX
 XX Claim 1; Fig 1; 178pp; English.
 XX
 XX AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus
 XX agalactiae) amino acid sequences of the invention. S. agalactiae is an
 XX encapsulated bacterium which is a major pathogen of humans causing sepsis
 XX and meningitis in neonates as well as adults. The S. agalactiae antigenic
 XX polypeptides are used to vaccinate against Group B Streptococcus
 XX infections, particularly to prevent infection in new born children
 XX arising from the maternal genital tract. An immunogenic composition is
 XX useful in the preparation of a medicament for the treatment or
 XX prophylaxis of Group B Streptococcus infection. The invention does not
 XX have the disadvantages of varied response rate associated with prior art

CC capsid polyeaccharide vaccination against Group B Streptococcus
XX Sequence 452 AA;
SQ

Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. NO. 4.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
||| |
Db 92 GYWLSAW 98

RESULT 4
ABU21589
ID ABU21589 standard; protein; 466 AA.
XX
AC ABU21589;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #7116.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Burkholderia fungorum.
XX
PN W0200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX N-PSDB; ACA25459.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 49513; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 466 AA;
SQ

Query Match 97.1%; Score 34; DB 6; Length 466;
Best Local Similarity 57.1%; Pred. NO. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
||| |
Db 86 GYWSAW 92

RESULT 5
ADS44861
ID ADS44861 standard; protein; 469 AA.
XX
AC ADS44861;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #23291.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 23291; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 469 AA;

Query Match 97.1%; Score 34; DB 8; Length 469;
 Best Local Similarity 57.1%; Pred. NO. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
 |||||
 Db 97 GYWVASW 103

RESULT 6
 ABU38334
 ID ABU38334 standard; protein; 472 AA.
 XX
 AC ABU38334;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #23861.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Pseudomonas aeruginosa.
 XX
 OS WO200277183-A2.
 XX
 PN 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.
 PF 21-MAR-2001; 2001US-00815242.
 XX 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 XX 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA42204.
 XX

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 66258; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 472 AA;

Query Match 97.1%; Score 34; DB 6; Length 472;
 Best Local Similarity 57.1%; Pred. NO. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
 |||||
 Db 94 GYWISAW 100

RESULT 7
 ABU24881
 ID ABU24881 standard; protein; 474 AA.

XX ABU24881;
 XX
 DT 19-JUN-2003 (first entry)
 XX

DE Protein encoded by Prokaryotic essential gene #10408.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Clostridium botulinum.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA28751.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 52805; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 474 AA;

Query Match 97.1%; Score 34; DB 6; Length 474;
Best Local Similarity 57.1%; Pred. NO. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 95 GYWLSAW 101

RESULT 8
ABP30560
ID ABP30560 standard; protein; 475 AA.

XX ABP30560;

XX 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 10296.

XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus agalactiae.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.

XX 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C;
PI Tettelin H;

XX WPI; 2002-352536/38.

DR N-PSDB; ABN71191.

XX New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.

XX Claim 1; Page 4161; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins

XX Sequence 475 AA;

Query Match 97.1%; Score 34; DB 5; Length 475;
Best Local Similarity 57.1%; Pred. NO. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 92 GYWLSAW 98

RESULT 9
ABU40245
ID ABU40245 standard; protein; 475 AA.

XX ABU40245;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #25772.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Pseudomonas putida.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

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PA (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA44115.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 68169; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 475 AA;
XX Query Match 97.1%; Score 34; DB 6; Length 475;
XX Best Local Similarity 57.1%; Pred. No. 4.6e+02;
XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 GYWXW 7
XX DB 93 GYWISAW 99
XX RESULT 10
XX ABU29756
XX ID ABU29756 standard; protein; 475 AA.
XX ABU29756;
XX AC ABU29756;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #15283.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Enterococcus faecium.
XX PN WO200277183-A2.
XX XX
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PD 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 23-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX N-PSDB; ACA33626.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 57680; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 475 AA;
XX Query Match 97.1%; Score 34; DB 6; Length 475;
XX Best Local Similarity 57.1%; Pred. No. 4.6e+02;
XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 GYWXW 7
XX DB 95 GYWLSAW 101
XX RESULT 11
XX ADS24700
XX ID ADS24700 standard; protein; 475 AA.
XX AC ADS24700;
XX XX
```

DT XX 02-DEC-2004 (first entry)
DE XX Bacterial polypeptide #13733.
KW XX Recombinant DNA construct; transformed plant; improved plant property;
KW XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW XX pathogen tolerance; pest tolerance; plant disease resistance;
KW XX cell cycle pathway modification; plant growth regulator;
KW XX homologous recombination; seed oil yield; protein yield; carbohydrate;
KW XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW XX bacterial polypeptide.
XX OS Bacteria.
XX XX US2003233675-A1.
XX PN 18-DEC-2003.
XX PD 20-FEB-2003; 2003US-00369493.
XX PF 21-FEB-2002; 2002US-03600399.
XX PR (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX FI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX DR WPI; 2004-061375/06.
XX DR New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 13733; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polypeptide used in the
XX CC scope of the invention. Note: The sequence data for this patent did not
XX CC form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX PS Sequence 475 AA;
XX CC Query Match 97.1%; Score 34; DB 8; Length 475;
XX CC Best Local Similarity 57.1%; Pred. No. 4.6e+02;
XX CC Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 12

ADV87906

XX ADV87906 standard; protein; 475 AA.
XX AC ADV87906;
XX DT 24-FEB-2005 (first entry)
XX XX Streptococcus agalactiae protein sequence, SEQ ID 300.
XX DE Antibacterial; Vaccine; bacterial infection.
XX KW Streptococcus agalactiae.
XX OS Streptococcus agalactiae.
XX PN FR2824074-A1.
XX PD 31-OCT-2002.
XX PF 26-APR-2001; 2001FR-00005642.
XX PR 26-APR-2001; 2001FR-00005642.
XX XX (INSP) INST PASTEUR.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX FI Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L,
XX PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu CP, Kunst F;
XX DR WPI; 2004-101891/11.
XX DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX PT agalactiae for the development of vaccines, diagnostic tools, DNA chips
XX PT and identification of therapeutic targets.
XX PS Claim 6; SEQ ID NO 300; 2687pp; French.

XX CC The present invention relates to novel Streptococcus agalactiae
XX CC nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II;
XX CC ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
XX CC agalactiae involved in the synthesis of amino acids, cell membranes,
XX CC intermediate (central) metabolism, energetic metabolism, fatty acid and
XX CC phospholipid metabolism, nucleotide metabolism including purines,
XX CC pyrimidines and/or nucleosides, regulatory functions, replication,
XX CC transcription, translation, protein transport, adaptation to atypical
XX CC conditions, sensitivity to medicines and/or analogues, functions related
XX CC to transporters, biosynthesis of cofactors, prosthetic groups and
XX CC transporters, cell membrane proteins and cellular machinery. (I) are
XX CC useful for the detection and/or amplification of nucleic acids.
XX CC Pharmaceutical composition comprising (I) or (II) are useful for
XX CC treatment of a bacterial S. agalactiae infection. Note: WO200292818A2 is
XX CC equivalent for the present basic patent FR2824074A1. WO200292818A2
XX CC contains 6617 sequence whereas the present patent only contains 2344
XX CC sequences.

XX PS Sequence 475 AA;

XX CC Query Match 97.1%; Score 34; DB 8; Length 475;

XX CC Best Local Similarity 57.1%; Pred. No. 4.6e+02;

XX CC Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX QY 1 GYWXW 7

XX DB 92 GYWLAW 98

RESULT 13

ADV81356

XX ADV81356 standard; protein; 475 AA.

XX AC ADV81356;

XX DT 24-FEB-2005 (first entry)

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XX DE Streptococcus agalactiae protein, SEQ ID 2497.
XX KW Antibacterial; vaccine; bacterial infection.
XX OS Streptococcus agalactiae.
XX PN WO200292818-A2.
XX PD 21-NOV-2002.
XX PF 26-APR-2002; 2002WO-IB003059.
XX PR 26-APR-2001; 2001FR-00005642.
XX PA (INSP ) INST PASTEUR.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
XX PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P, Kunst F;
XX WPI; 2004-101891/11.
XX DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX PT agalactiae for the development of vaccines, diagnostic tools, DNA chips
XX PT and identification of therapeutic targets.
XX PS Claim 6; SEQ ID NO 2497; 439pp; French.
XX CC The present invention relates to novel Streptococcus agalactiae
XX CC nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
XX CC novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
XX CC nucleotide sequences encode polypeptides of S. agalactiae involved in the
XX CC synthesis of amino acids, cell membranes, intermediate (central)
XX CC metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
XX CC nucleotide metabolism including purines, pyrimidines and/or nucleosides,
XX CC regulatory functions, replication, transcription, translation, protein
XX CC transport, adaptation to atypical conditions, sensitivity to medicines
XX CC and/or analogues, functions related to transporters, cell membrane proteins and
XX CC cofactors, prosthetic groups and transporters, cell membrane proteins and
XX CC of nucleic acids. Pharmaceutical composition comprising (I) or (II) are
XX CC useful for treatment of a bacterial S. agalactiae infection. The complete
XX CC genome of Streptococcus agalactiae is given in ADV81204. Note: The
XX CC present patent is an equivalent for the basic patent FR2824074A1, which
XX CC contains only 2344 sequences.
XX SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
   |||||
Db 92 GYWLSAW 98

RESULT 14
ADV79159
ID ADV79159 standard; protein; 475 AA.
XX AC ADV79159;
XX XX
XX DT 24-FEB-2005 (first entry)
XX DE Streptococcus agalactiae protein, SEQ ID 300.
XX KW Antibacterial; vaccine; bacterial infection.
XX OS Streptococcus agalactiae.
XX PN WO200292818-A2.

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
   |||||
Db 92 GYWLSAW 98

RESULT 15
ADC97241
ID ADC97241 standard; protein; 478 AA.
XX AC ADC97241;
XX XX
XX DT 01-JAN-2004 (first entry)
XX DE E. faecium protein sequence SEQ ID 6868.
XX KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
XX KW abdominal-pelvic infection.
XX OS Enterococcus faecium.
XX PN US6583275-B1.
XX XX
XX PD 24-JUN-2003.
XX PF 30-JUN-1998; 98US-00107532.
XX PR 02-JUL-1997; 97US-0051571P.
XX PR 14-MAY-1998; 98US-0085598P.

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XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA
XX PI
XX Doucette-Stamm LA, Bush D;
XX WPI; 2003-799836/75.
XX DR N-PSDB; ADC93587.
XX DR
XX PT
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
XX Enterococcus faecium polypeptide useful for detection, prevention and
XX treatment of a pathological condition resulting from a bacterial
XX infection.
XX Example 1; SEQ ID NO 6868; 243pp; English.
XX
XX The invention relates to an isolated nucleic acid derived from
XX Enterococcus faecium encoding an Enterococcus faecium polypeptide having
XX one of 10 fully defined sequences given in the (or comprising 40
XX sequential nucleotides chosen from any of the nucleic acids, its
XX complement or sequences hybridising to it). Also included are a
XX recombinant vector comprising the nucleic acid operably linked to
XX transcription regulatory element, a cell comprising the vector and a
XX single-stranded probe comprising the nucleic acid. The nucleic acids are
XX chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
XX The nucleic acids are useful for diagnosing pathological conditions
XX resulting from E. faecium bacterial infection (e.g. urinary tract
XX infection, bacteraemia, endocarditis, wounds and abdominal pelvic
XX infection) and for screening drugs such as agonists and antagonists. The
XX nucleic acid is useful for recombinant production of Candida albicans
XX derived peptides or antisense polypeptides. Pharmaceutical compositions
XX and vaccines containing the nucleic acid are useful for preventing or
XX treating Enterococcus faecium infections. The present sequence represents
XX one if the disclosed E. faecium proteins.
XX
XX SQ Sequence 478 AA;
XX Query Match 97.1%; Score 34; DB 7; Length 478;
XX Best Local Similarity 57.1%; Pred. No. 4.7e+02;
XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GYWXXXW 7
XX |||
XX Db 98 GYLSSAW 104
XX
XX Search completed: May 2, 2006, 08:54:54
XX Job time : 93.2326 secs
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 14.5116 Seconds

(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 35

Sequence: 1 GYWXXXW 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: Piri.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	97.1	72	T03190	hypothetical prote
2	34	97.1	108	S12193	hypothetical prote
3	34	97.1	345	T37139	hypothetical prote
4	34	97.1	469	D70048	ABC transporter (a
5	34	97.1	472	E83497	probable amino aci
6	34	97.1	475	T46745	arginine/ornithine
7	34	97.1	482	JH0110	arginine/ornithine
8	34	97.1	490	C86879	arginine/ornithine
9	34	97.1	497	C86878	ig heavy chain pre
10	33	94.3	142	C34903	CDPdiacylglycerol
11	33	94.3	227	T37905	hypothetical prote
12	33	94.3	250	A69843	oligopeptide ABC t
13	33	94.3	289	G72215	hypothetical prote
14	33	94.3	360	A22047	probable transport
15	33	94.3	441	C95307	probable ABC trans
16	33	94.3	508	C95282	hypothetical prote
17	33	94.3	517	A13201	probable carbohydr
18	33	94.3	519	E83268	hypothetical prote
19	33	94.3	534	T15414	probable dipeptide
20	33	94.3	535	B95952	hypothetical prote
21	33	94.3	541	AC2392	hypothetical prote
22	33	94.3	563	AH2975	oPhA protein limpo
23	33	94.3	563	C98307	hypothetical prote
24	33	94.3	592	T15413	hypothetical prote
25	33	94.3	778	T31037	multidrug resistan
26	33	94.3	1502	T42216	lysis protein S -
27	32	91.4	71	S22905	hypothetical prote
28	32	91.4	83	E69903	hypothetical prote
29	32	91.4	187	G83047	hypothetical prote

30	32	91.4	218	2	S76385	hypothetical prote
31	32	91.4	218	2	D87264	hypothetical prote
32	32	91.4	257	2	E75325	probable mscf prot
33	32	91.4	261	2	JC5806	aquaporin 8 - mous
34	32	91.4	263	2	JC5622	aquaporin 8 - rat
35	32	91.4	271	2	F83188	phosphatidate cyti
36	32	91.4	271	2	JC4832	phosphatidate cyti
37	32	91.4	282	2	H95869	probable sugar ABC
38	32	91.4	286	2	E88690	protein F41H10.7 (
39	32	91.4	344	2	C82611	hypothetical prote
40	32	91.4	447	2	H97146	siderophore/surfac
41	32	91.4	448	2	AB0301	conserved hypotet
42	32	91.4	466	2	T35164	probable secreted
43	32	91.4	519	2	S75572	oligopeptide trans
44	32	91.4	536	2	G95389	probable ABC trans
45	32	91.4	631	2	B86233	hypothetical prote

ALIGNMENTS

RESULT 1

T03190

hypothetical protein 72B - rice mitochondrion

C:Species: mitochondrion Oryza sativa (rice)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: T03190

R:Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.

Plant Cell Physiol. 35, 1239-1244, 1994

A:Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existe

A:Reference number: Z14841; MUID:95211382; PMID:7545979

A:Accession: T03190

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-72 <ITA>

A:Cross-references: UNIPROT:Q35302; UNIPARC:UPI000009746F; EMBL:D32052; NID:G769704; P

A:Experimental source: cultivar Nipponbare

C:Genetics:

A:Genome: mitochondrion

C:Keywords: mitochondrion

Query Match 97.1%; Score 34; DB 2; Length 72;

Best Local Similarity 57.1%; Pred. No. 14;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

Db 34 GYWSSHW 40

RESULT 2

S12193

hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTf1

C:Species: Thiobacillus ferrooxidans

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S12193

R:Drolet, M.; Zanga, P.; Lau, P.C.K.

Mol. Microbiol. 4, 1381-1391, 1990

A:Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidan

A:Reference number: S12188; MUID:91125140; PMID:2280689

A:Accession: S12193

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-108 <DRO>

A:Cross-references: UNIPROT:P20088; UNIPARC:UPI000013B9EC; EMBL:X52699; NID:G48158; PI

C:Genetics:

A:Genome: plasmid pTf1

Query Match 97.1%; Score 34; DB 2; Length 108;

Best Local Similarity 57.1%; Pred. No. 21;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

```
Db      89 GYWRSSW 95
|||||
RESULT 3
T37139
Hypothetical protein SCU9A.03c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37139
R:Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21622
A:Accession: T37139
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <HAR>
A:Cross-references: UNIPROT:Q9S1R7; UNIPARC:UPI00000DB3A4; EMBL:AL109972; PIDN:CAB53264.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEBA:SCU9A.03c
C:Superfamily: Streptomyces coelicolor hypothetical protein SCU9A.03c

Query Match      97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXKXW 7
      |||||
Db      147 GYWAARW 153

RESULT 4
D70048
ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C:Accession: D70048
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Boudillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
A:Authors: Koenigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Koetter, P.; Koenigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaite, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70048
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-469 <KUN>
A:Cross-references: UNIPROT:Q32204; UNIPARC:UPI0000060A54; GB:Z99121; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvsh
C:Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXKXW 7
      |||||
Db      97 GYWAASW 103

RESULT 5
E83497
Probable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: E83497
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; E
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <STO>
A:Cross-references: UNIPROT:O914E4; UNIPARC:UPI00000C529E; GB:AE004549; GB:AE004091; NI
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1194
C:Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 472;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXKXW 7
      |||||
Db      94 GYWISAW 100

RESULT 6
T46745
Arginine/ornithine antiporter [imported] - Lactobacillus sakei
C:Species: Lactobacillus sakei
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C:Accession: T46745
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez,
J. Bacteriol. 180, 4154-4159, 1998
A:title: Structural and functional analysis of the gene cluster encoding the enzymes of
A:Reference number: Z23141; MUID:98361904; PMID:9696763
A:Accession: T46745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <ZUN>
A:Cross-references: UNIPROT:O53092; UNIPARC:UPI0000125DAC; EMBL:AJ001330; NID:92764610;
C:Genetics:
A:Gene: arcD
C:Function:
A:Description: necessary for arginine transport; involved in ornithine-arginine exchang
A:Pathway: arginine catabolism
C:Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 475;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXKXW 7
      |||||
Db      94 GYWLSAW 100

RESULT 7
JH0110
Arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004
C:Accession: JH0110; A82999
R:Luethi, E.; Baur, H.; Gampel, M.; Brunner, P.; Villevall, D.; Mercenier, A.; Haas, D.
Gene 87, 37-43, 1990
A:title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cor
A:Reference number: JH0110; MUID:90236296; PMID:2158926
A:Accession: JH0110
```

A:Molecule type: DNA
A:Residues: 1-482 <LUE>
A:Cross-references: UNIPROT:P18275; UNIPARC:UPI00000618AA; GB:AE005176; PID:g12725079;
A:Experimental source: strain PA01
A:Note: the gene encoding this protein is located upstream of the arcABC genes which end
R:Stover, C.K.; Pham, X.O.; Erwin, A.B.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A82959
A:Molecule type: DNA
A:Residues: 1-482 <STO>
A:Cross-references: UNIPARC:UPI00000618AA; GB:AE004930; NID:g9951472; PID:
A:Experimental source: strain PA01
A:Genetics:
A:Gene: arcD; PA5170
A:Superfamily: ecotropic retrovirus receptor protein
C:Keywords: transmembrane protein

Query Match 97.1%; Score 34; DB 2; Length 482;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 94 GYWISAW 100

RESULT 8
C86879
arginine/ornithine antiporter [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL140
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C:Accession: C86879
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86879
A:Molecule type: DNA
A:Residues: 1-490 <STO>
A:Cross-references: UNIPROT:Q9CE15; UNIPARC:UPI000006B99; GB:AE005176; PID:g12725084; F
A:Experimental source: strain IL1403
A:Genetics:
A:Gene: arcD1
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 97.1%; Score 34; DB 2; Length 490;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 93 GYWISAW 99

RESULT 9
C86878
arginine/ornithine antiporter [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL140
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C:Accession: G86878
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86878
A:Molecule type: DNA

A:Residues: 1-497 <STO>
A:Cross-references: UNIPROT:Q9CE19; UNIPARC:UPI000006B95; GB:AE005176; PID:g12725079;
A:Experimental source: strain IL1403
A:Genetics:
A:Gene: arcD2
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 97.1%; Score 34; DB 2; Length 497;
Best Local Similarity 57.1%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 93 GYWISAW 99

RESULT 10
C34903
Ig heavy chain precursor V region (5-27) - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C:Accession: C34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-r
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: C34903
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-142 <BED>
A:Cross-references: UNIPARC:UPI0000176COP
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMW>

Query Match 94.3%; Score 33; DB 2; Length 142;
Best Local Similarity 57.1%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 126 GYWFAYW 132

RESULT 11
S73905
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) pgsA - M
N:Alternate names: hypothetical protein A65_orf227
C:Species: *Mycoplasma pneumoniae*
A:Variety: ATCC 29342
C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S73905
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumonia*
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73905
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-227 <HIM>
A:Cross-references: UNIPROT:P75520; UNIPARC:UPI0000131886; EMBL:AE000057; GB:U000089; N
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Gene: pgsA
A:Genetic code: SGC3
C:Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C:Keywords: transferase

Query Match 94.3%; Score 33; DB 2; Length 227;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

```
Db      84 GYWAREK.90

RESULT 12
A:Species: Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69843
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chhabra, A.; Ehrlich, S.D.; Emmerman, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Fulgider, D.R.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Levine, A.; Liu, H.; Maeda, S.; Mausel, Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaite, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron, akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69843
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-250 <KUN>
A:Cross-references: UNIPROT:O31597; UNIPARC:UPI0000060207; GB:299110; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yjba
C:Superfamily: Bacillus subtilis hypothetical protein yjba

Query Match      94.3%; Score 33; DB 2; Length 250;
Best Local Similarity 57.1%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 185 GYWTW 191

RESULT 13
G72215
Oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: G72215
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72215
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <ARN>
A:Cross-references: UNIPROT:Q9X270; UNIPARC:UPI000000385E; GB:AE001813; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1748
C:Superfamily: oligopeptide permease protein oppB

Query Match      94.3%; Score 33; DB 2; Length 289;
Best Local Similarity 57.1%; Pred. No. 75;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 185 GYWTW 191

RESULT 14
A:Species: Nostoc sp. PCC 7120 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A:Note: Nostoc sp. #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2047
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <KUR>
A:Cross-references: UNIPROT:O8YVP3; UNIPARC:UPI000000CE269; GB:BA000019; PIDN:BA073630.1
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1931

Query Match      94.3%; Score 33; DB 2; Length 360;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 127 GYWSY 133

RESULT 15
C95307
Probable transport protein SMA0684 [imported] - Sinorhizobium meliloti (strain 1021) m
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 05-Oct-2004
C:Accession: C95307
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bo Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melil
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95307
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <KUR>
A:Cross-references: UNIPROT:Q92ZT6; UNIPARC:UPI000000CB08F; GB:AE006469; PIDN:AAK65021.1
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, i
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMA0684
A:Genome: plasmid
C:Superfamily: ecotropic retrovirus receptor protein

Query Match      94.3%; Score 33; DB 2; Length 441;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 92 GYWSY 98
```

us-10-046-922-68.rpr

Tue May 2 12:32:43 2006

Search completed: May 2, 2006, 08:56:18
Job time : 17.5116 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.6047 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYWXWXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	72	Q35302_ORYSA	Q35302 oryza sativ
2	34	97.1	108	YML2_THIFE	P20088 thiobacilli
3	34	97.1	130	Q7U395_PROMP	Q7U395 prochloroco
4	34	97.1	236	Q9WGW9_9HIV1	Q9WGW9 human immun
5	34	97.1	253	Q32816_LACLC	Q32816 lactococcus
6	34	97.1	294	Q8ET30_OCEIH	Q8ET30 oceanobacill
7	34	97.1	333	Q6F6U4_ACIAH	Q6F6U4 acinetobact
8	34	97.1	345	Q9SIR7_STRCO	Q9SIR7 streptomyce
9	34	97.1	451	Q62C74_BURMA	Q62C74 burkholderi
10	34	97.1	459	Q84DL5_OENOE	Q84DL5 enococcus
11	34	97.1	464	Q613F7_BACAN	Q613F7 bacillus an
12	34	97.1	465	Q4MN56_BACCE	Q4MN56 bacillus ce
13	34	97.1	465	Q81H27_BACCR	Q81H27 bacillus ce
14	34	97.1	465	Q63G16_BACCH	Q63G16 bacillus th
15	34	97.1	465	Q8HNI4_BACHK	Q8HNI4 bacillus th
16	34	97.1	465	Q73DL5_BACCL	Q73DL5 bacillus ce
17	34	97.1	465	Q81V71_BACAN	Q81V71 bacillus an
18	34	97.1	467	Q65F15_BACLD	Q65F15 bacillus li
19	34	97.1	467	Q6TK71_STRTR	Q6TK71 streptococ
20	34	97.1	469	Q32204_BACSU	Q32204 bacillus su
21	34	97.1	469	Q8HP27_BACHK	Q8HP27 bacillus th
22	34	97.1	471	Q73E85_BACCL	Q73E85 bacillus ce
23	34	97.1	471	Q81IH9_BACCR	Q81IH9 bacillus ce
24	34	97.1	471	Q914E4_PSEAE	Q914E4 pseudomonas
25	34	97.1	472	Q81H27_BACCR	Q81H27 bacillus ce
26	34	97.1	473	Q7NRJ8_CHRVO	Q7NRJ8 chromobacte
27	34	97.1	475	1 ARCD_LACSK	053092 lactobacill
28	34	97.1	475	Q4ZT00_PSESY	Q4ZT00 pseudomonas
29	34	97.1	475	Q4K7R6_PSEF5	Q4K7R6 pseudomonas
30	34	97.1	475	Q4K7R5_PSEF5	Q4K7R5 pseudomonas
31	34	97.1	475	Q88P50_PSEPK	Q88P50 pseudomonas

32	34	97.1	475	2	Q88P51_PSEPK	Q88P51 pseudomonas
33	34	97.1	475	2	Q8DWP9_STRAS	Q8DWP9 streptococc
34	34	97.1	475	2	Q8E2J7_STRAS	Q8E2J7 streptococc
35	34	97.1	478	1	ARCD_CLOPE	Q46170 clostridium
36	34	97.1	482	1	ARCD_PSEAE	P18275 pseudomonas
37	34	97.1	486	2	Q63U74_BURPS	Q63U74 burkholderi
38	34	97.1	486	2	Q62KE0_BURMA	Q62KE0 burkholderi
39	34	97.1	490	2	Q9CE15_LACLA	Q9CE15 lactococcus
40	34	97.1	496	2	Q63L96_BURPS	Q63L96 burkholderi
41	34	97.1	497	2	Q9KGV0_LACLA	Q9KGV0 lactococcus
42	34	97.1	497	2	Q9CE19_LACLA	Q9CE19 lactococcus
43	34	97.1	526	2	Q9K574_9LACT	Q9K574 lactococcus
44	34	97.1	552	2	Q5LSW7_SILPO	Q5LSW7 silicibacte
45	34	97.1	753	2	Q4TSN3_9SPHN	Q4TSN3 erythrobact

ALIGNMENTS

RESULT 1
Q35302_ORYSA PRELIMINARY; PRT; 72 AA.
AC Q35302;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE ORF72B.
OS Oryza sativa (japonica cultivar-group).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,
RA Li'in Y.V.;
RT "Structure of long and short copies of the mobile dispersed gene MDG3
of Drosophila melanogaster.";
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95308541; PubMed=7788722; DOI=10.1007/BF00313433;
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiyura M.,
RA Hirai A.;
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is
transcribed from alternative promoters.";
RL Curr. Genet. 27:184-189(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95211382; PubMed=7545979;
RA Itadani H., Wakasugi T., Sugita M., Sugiyura M., Nakazono M., Hirai A.;
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:
the existence of many sequences that correspond to parts of
mitochondrial genes in intergenic regions.";
RL Plant Cell Physiol. 35:1239-1244(1994).
DR EMBL; D32052; BAA06811.1; -; Genomic_DNA.
DR PIR; T03190; T03190.
DR Gramene; Q35302; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 72 AA; 8155 MW; D42DE53BED28432E CRC64;

Query Match 97.1%; Score 34; DB 2; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXWXX 7
DB 34 GYWSWW 40

RESULT 2

```
YML2_THIFE
ID YML2_THIFE STANDARD; PRT; 108 AA.
AC P2008;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical 12.3 kDa protein in mobL 3' region (ORF 4).
OS Thiobacillus ferrooxidans.
OG Plasmid pTF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drolet M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
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CC removed.
CC -----
CC DR EMBL; X52699; CAA36930.1; -; Genomic_DNA.
CC PR; S12193; S12193.
CC KW Hypothetical protein; plasmid.
CC SQ SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;

Query Match 97.1%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 89 GYWRSS 95

RESULT 3
Q7U395_PROMP PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible Adenoviral fiber protein (Repeat/shaf).
GN OrderedLocusNames=PM1067;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus
OX NCBI_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
RL Nature 424:1042-1047(2003).
RL EMBL; BX572092; CAG19526.1; -; Genomic_DNA.
RW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; E0F4A997FCA8CDB CRC64;

Query Match 97.1%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

YML2_THIFE
ID YML2_THIFE STANDARD; PRT; 108 AA.
AC P2008;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical 12.3 kDa protein in mobL 3' region (ORF 4).
OS Thiobacillus ferrooxidans.
OG Plasmid pTF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drolet M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
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CC removed.
CC -----
CC DR EMBL; X52699; CAA36930.1; -; Genomic_DNA.
CC PR; S12193; S12193.
CC KW Hypothetical protein; plasmid.
CC SQ SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;

Query Match 97.1%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 89 GYWRSS 95

RESULT 3
Q7U395_PROMP PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible Adenoviral fiber protein (Repeat/shaf).
GN OrderedLocusNames=PM1067;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus
OX NCBI_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
RL Nature 424:1042-1047(2003).
RL EMBL; BX572092; CAG19526.1; -; Genomic_DNA.
RW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; E0F4A997FCA8CDB CRC64;

Query Match 97.1%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GYWXW 7
DB 7 GYWTAW 13

RESULT 4
Q9WGW9_9HIV1 PRELIMINARY; PRT; 236 AA.
ID Q9WGW9_9HIV1 PRELIMINARY; PRT; 236 AA.
AC Q9WGW9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OG Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
mother to infant.";
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121641; AAD29013.1; -; Genomic_DNA.
DR HSSP; P03366; 1HRH.
DR SMR; Q9WGW9; 1-236.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR010659; RVT_connect.
DR InterPro; IPR010661; RVT_thumb.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
DR PROSITE; PS50879; RNaseH; 1.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 236
SQ SEQUENCE 236 AA; 27062 MW; 24D6BB0409A80BB8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 236;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 129 GYWTAW 135

RESULT 5
O32816_LACLC PRELIMINARY; PRT; 253 AA.
ID O32816_LACLC PRELIMINARY; PRT; 253 AA.
AC O32816;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine/ornithine antiporter homolog ArcD (Fragment).
GN Name=arcD;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
```

RESULT 7
Q6F6U4 ACIAD
ID O6F6U4 ACIAD PRELIMINARY: PRT: 333 AA.

11]	—
RN	NUCLEOTIDE SEQUENCE.
RP	
RC	STRAIN=AS3(2) / M145;
RK	MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RX	Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis H.,
RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Kessler H.,
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA	Arinon A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA	Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA	Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Ruter S.,
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA	Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA	Hopwood D.A.;
RT	"Complete genome sequence of the model actinomycete Streptomyces
RT	coelicolor A3(2).";
RL	Nature417:141-147(2002).
RL	EMBL; AJ39104; CAB53264.1; -; Genomic_DNA.
DR	PIR; T37139; T37139.
DR	Complete proteome; Hypothetical protein.
DR	SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;
SK	


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Query Match          97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
    |||
Db 147 GYWAARW 153

RESULT 9
Q62C74_BURMA
ID Q62C74_BURMA PRELIMINARY; PRT; 451 AA.
AC Q62C74;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Amino acid permease.
GN OrderedLocNames=BMAA1038;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dmitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000011; AAU46467.1; -; Genomic_DNA.
DR TIGR; BMAA1038; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 451 AA; 47344 MW; ED2D1ADBE0C4A55 CRC64;

Query Match          97.1%; Score 34; DB 2; Length 451;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
    |||
Db 116 GYWSAW 122

RESULT 10
Q9KGV3_LACLA
ID Q9KGV3_LACLA PRELIMINARY; PRT; 459 AA.
AC Q9KGV3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 26, Last annotation update)
DE ArcD1.
GN Name=arcD1;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ML3;
RC Chou L., Weimer B., Xie Y.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL

Query Match          97.1%; Score 34; DB 2; Length 464;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
    |||
Db 94 GYWLSSW 100

RESULT 12
Q613F7_BACAN
ID Q613F7_BACAN PRELIMINARY; PRT; 465 AA.
AC Q613F7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
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05-JUL-2004 (TReMBLrel. 27, Last sequence update)
05-JUL-2004 (TReMBLrel. 27, Last annotation update)
Amino acid permease family protein.
OrderedLocusNames=BAS0596;
Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
NCBI_TaxID=1392;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterner;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017225; AAT52924.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR0042293; AA/permease.
DR Pfam; PF00324; AA/permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 96 GYWAANW 102

RESULT 13
Q4MN56_BACCE PRELIMINARY; PRT; 465 AA.
AC Q4MN56;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Arginine/ornithine antiporter.
GN Name=arcD; ORFNames=BCE_G9241_0606;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
NCBI_TaxID=269801;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RA Hoffmester A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
with an illness resembling inhalation anthrax."
Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AA001000024; EAL13575.1; -; Genomic_DNA.
SQ SEQUENCE 465 AA; 50180 MW; F2A1540B055C90B9 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 96 GYWAANW 102

us-10-046-922-68.rup

05-JUL-2004 (TReMBLrel. 27, Last sequence update)
05-JUL-2004 (TReMBLrel. 27, Last annotation update)
Amino acid permease family protein.
OrderedLocusNames=BAS0596;
Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
NCBI_TaxID=1392;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterner;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017225; AAT52924.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR0042293; AA/permease.
DR Pfam; PF00324; AA/permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 96 GYWAANW 102

RESULT 14
Q81HZ7_BACCR PRELIMINARY; PRT; 465 AA.
AC Q81HZ7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Arginine/ornithine antiporter.
GN OrderedLocusNames=BC0629;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
NCBI_TaxID=226900;
[1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AB017000; AAP07646.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease.
DR Pfam; PF00324; AA/permease; 1.
KW Complete proteome.
SQ SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 96 GYWAANW 102

RESULT 15
Q63G16_BACCCZ PRELIMINARY; PRT; 465 AA.
AC Q63G16;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Probable arginine/ornithine antiporter protein.
GN Name=arcD;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
NCBI_TaxID=288681;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CP000001; AAU19700.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.

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DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR InterPro: IPR004841; Permease region.
DR Pfam: PF00324; AA_Permease: 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50178 MW; 55D7083AAE7B3958 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
||| |
Db 96 GYWAANW 102

Search completed: May 2, 2006, 08:46:43
Job time : 93.6047 secs


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Query Match          97.1%; Score 34; DB 2; Length 478;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7
   |||
Db 98 GYWSAW 104

RESULT 2
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328

Query Match          97.1%; Score 34; DB 2; Length 499;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7
   |||
Db 111 GYWSAW 117

RESULT 3
US-09-252-991A-19339
; Sequence 19339, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19339
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19339

Query Match          97.1%; Score 34; DB 2; Length 865;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7
   |||
Db 487 GYWSAW 493

RESULT 4
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US-09-252-991A-18697
; Sequence 18697, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18697
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18697

Query Match          94.3%; Score 33; DB 2; Length 543;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7
   |||
Db 331 GYWMVSW 337

RESULT 5
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792.616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match          94.3%; Score 33; DB 2; Length 1498;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7
   |||
Db 960 GYWLW 966

RESULT 6
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792.616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
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Tue May 2 12:32:42 2006

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; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-792-616-3

Query Match      94.3%; Score 33; DB 2; Length 1503;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
Db      965 GYWLSW 971

RESULT 7
US-09-647-140B-8
; Sequence 8, Application US/09647140B
; Patent No. 6803184
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: WRP-Related ABC Transporter Encoding
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: US/09/647,140B
; CURRENT FILING DATE: 2001-05-21
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-647-140B-8

Query Match      94.3%; Score 33; DB 2; Length 1503;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
Db      965 GYWLSW 971

RESULT 8
US-09-902-540-12675
; Sequence 12675, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12675
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Myxococcus xanthus

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US-09-902-540-12675

Query Match      91.4%; Score 32; DB 2; Length 88;
Best Local Similarity 57.1%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
Db      48 GYWLDGW 54

RESULT 9
US-09-543-681A-7620
; Sequence 7620, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB.
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7620
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-7620

Query Match      91.4%; Score 32; DB 2; Length 177;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
Db      43 GYWINW 49

RESULT 10
US-09-502-653-10
; Sequence 10, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schleim, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481.200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Bacillus circulans
; US-09-502-653-10

Query Match      91.4%; Score 32; DB 2; Length 252;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;

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Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
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Db 210 GYWEPAW 216

RESULT 11

US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klinger, Tod M.
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT
; FILE REFERENCE: PC-0012 CIP
; CURRENT APPLICATION NUMBER: US/09/610,906
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 09/226,994
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. 6566066: 92346968
; PUBLICATION INFORMATION:
US-09-610-906-12

Query Match 91.4%; Score 32; DB 2; Length 263;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
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Db 224 GYWDPMW 230

RESULT 12

US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15791
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791

Query Match 91.4%; Score 32; DB 2; Length 274;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 84 GYWPITW 90

RESULT 13

US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match 91.4%; Score 32; DB 2; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 108 GYWIPLW 114

RESULT 14

US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match 91.4%; Score 32; DB 2; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 108 GYWIPLW 114

RESULT 15

US-09-624-670-17
; Sequence 17, Application US/09624670

Tue May 2 12:32:42 2006

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; Patent No. 6913916
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P2
; CURRENT APPLICATION NUMBER: US/09/624,670
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-624-670-17

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Query Match          91.4%; Score 32; DB 2; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 GYWXXXW 7
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Db      108 GYWIFLW 114

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Search completed: May 2, 2006, 08:58:25
Job time : 23.6977 secs

Tue May 2 12:32:43 2006

us-10-046-922-68.rapbm

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 74.4186 Seconds
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Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYWXWXX 8

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	58	4	US-10-425-115-308836
2	34	97.1	72	4	US-10-437-963-176036
3	34	97.1	452	4	US-10-091-007-88
4	34	97.1	466	4	US-10-282-122A-49513
5	34	97.1	469	4	US-10-369-493-23291
6	34	97.1	472	4	US-10-282-122A-66258
7	34	97.1	474	4	US-10-282-122A-52805
8	34	97.1	475	4	US-10-369-493-13733
9	34	97.1	475	4	US-10-282-122A-57680
10	34	97.1	475	4	US-10-282-122A-68169
11	34	97.1	506	4	US-10-282-122A-50338
12	34	97.1	585	3	US-09-894-018-87
13	34	97.1	585	5	US-10-474-960A-87
14	33	94.3	10	4	US-10-046-922-34
15	33	94.3	10	4	US-10-046-922-35
16	33	94.3	47	4	US-10-425-115-287762
17	33	94.3	104	4	US-10-425-115-273234
18	33	94.3	116	3	US-09-910-483-1
19	33	94.3	116	3	US-09-910-483-5
20	33	94.3	116	3	US-09-910-483-9
21	33	94.3	116	3	US-09-910-483-13
22	33	94.3	116	3	US-09-910-483-17
23	33	94.3	116	3	US-09-910-483-21
24	33	94.3	116	3	US-09-910-483-25
25	33	94.3	116	3	US-09-910-483-29
26	33	94.3	116	3	US-09-910-483-33
27	33	94.3	116	3	US-09-910-483-37

Sequence 41, Appl
Sequence 43, Appl
Sequence 357518
Sequence 86, Appl
Sequence 90, Appl
Sequence 64263, A
Sequence 344695, A
Sequence 43035, A
Sequence 9632, Ap
Sequence 19811, A
Sequence 16537, A
Sequence 199114, A
Sequence 7, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 2, Appl
Sequence 17, Appl
Sequence 2, Appl

28 33 94.3 116 3 US-09-910-483-41
29 33 94.3 116 3 US-09-910-483-43
30 33 94.3 129 4 US-10-425-115-357518
31 33 94.3 138 4 US-10-160-232-86
32 33 94.3 138 4 US-10-160-232-90
33 33 94.3 227 4 US-10-282-122A-64263
34 33 94.3 229 4 US-10-425-115-344695
35 33 94.3 229 4 US-10-450-763-43035
36 33 94.3 257 5 US-10-450-763-43035
37 33 94.3 296 4 US-10-158-761-9632
38 33 94.3 296 4 US-10-369-493-16537
39 33 94.3 466 4 US-10-369-493-16537
40 33 94.3 466 4 US-10-437-963-199114
41 33 94.3 516 4 US-10-450-022-7
42 33 94.3 526 4 US-10-450-022-4
43 33 94.3 526 4 US-10-450-022-5
44 33 94.3 526 5 US-10-450-185B-2
45 33 94.3 526 5 US-10-450-185B-17
45 33 94.3 526 5 US-10-433-747B-2

ALIGNMENTS

RESULT 1
US-10-425-115-308836
; Sequence 308836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 308836
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_44726C.1.pap
US-10-425-115-308836

Query Match 97.1%; Score 34; DB 4; Length 58;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXWXX 7
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Db 49 GYWGASW 55

RESULT 2
US-10-437-963-176036
; Sequence 176036, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Fang
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176036
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pap
US-10-437-963-176036

Query Match 97.1%; Score 34; DB 4; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
DB 34 GYWSW 40

RESULT 3

US-10-091-007-88
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited Wells, Jeremy M
; APPLICANT: Le Page, Richard W F
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88

Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
DB 92 GYWSW 98

RESULT 4

US-10-282-122A-49513
; Sequence 49513, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49513
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49513

Query Match 97.1%; Score 34; DB 4; Length 466;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
DB 86 GYWSW 92

RESULT 5

US-10-369-493-23291
; Sequence 23291, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23291

Query Match 97.1%; Score 34; DB 4; Length 469;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
DB 97 GYWSW 103

RESULT 6

US-10-282-122A-66258
; Sequence 66258, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

us-10-046-922-68.rapbm

Tue May 2 12:32:43 2006

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; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66258
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-10-282-122A-66258

Query Match          97.1%; Score 34; DB 4; Length 472;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
Db 94 GYWISAW 100

RESULT 7
US-10-282-122A-52805
; Sequence 52805, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52805
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Clostridium botulinum
; US-10-282-122A-52805

Query Match          97.1%; Score 34; DB 4; Length 474;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
Db 95 GYWLAW 101

RESULT 8
US-10-369-493-13733
; Sequence 13733, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13733
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
; US-10-369-493-13733

Query Match          97.1%; Score 34; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
Db 93 GYWLAW 99

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RESULT 9

US-10-282-122A-57680
; Sequence 57680, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 57680

LENGTH: 475

TYPE: PRT

ORGANISM: Enterococcus faecium

US-10-282-122A-57680

Query Match 97.1%; Score 34; DB 4; Length 475;

Best Local Similarity 57.1%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

1 GYWXW 7

|||

95 GYWLSAW 101

RESULT 10

US-10-282-122A-68169

; Sequence 68169, Application US/10282122A

; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 68169

LENGTH: 475

TYPE: PRT

ORGANISM: Pseudomonas putida

US-10-282-122A-68169

Query Match 97.1%; Score 34; DB 4; Length 475;

Best Local Similarity 57.1%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

1 GYWXW 7

|||

93 GYWLSAW 99

RESULT 11

US-10-282-122A-50338

; Sequence 50338, Application US/10282122A

; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50338
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50338

Query Match
Best Local Similarity 97.1%; Score 34; DB 4; Length 506;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 124 GYWISAW 130

RESULT 12
US-09-894-018-87
; Sequence 87, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc..
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denise
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39863-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
US-09-894-018-87

Query Match
Best Local Similarity 97.1%; Score 34; DB 3; Length 585;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 22 GYWOATW 28

US-09-894-018-87

Query Match
Best Local Similarity 97.1%; Score 33; DB 4; Length 10;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 22 GYWOATW 28

RESULT 13
US-10-474-960A-87
; Sequence 87, Application US/10474960A
; Publication No. US20040248113A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denise
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
; FILE REFERENCE: 2060.0320004
; CURRENT APPLICATION NUMBER: US/10/474,960A
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/US02/09877
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/894,018
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
US-10-474-960A-87

Query Match
Best Local Similarity 97.1%; Score 34; DB 5; Length 585;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 22 GYWOATW 28

RESULT 14
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match
Best Local Similarity 97.1%; Score 33; DB 4; Length 10;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 22 GYWOATW 28
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Db ||| |
 2 GYWLTIW 8

RESULT 15
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match 94.3%; Score 33; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXYW 7
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Db 2 GYWLTIW 8

Search completed: May 2, 2006, 09:32:38
Job time : 75.4186 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17 ; Search time 11.3488 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYWXWXXW 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
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2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS5/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
7: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
8: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
10: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	464	11	US-11-087-099-1003
2	34	97.1	469	11	US-11-087-099-11321
3	34	97.1	471	11	US-11-188-298-19864
4	34	97.1	472	11	US-11-087-099-12291
5	34	97.1	475	11	US-11-087-099-1870
6	34	97.1	475	11	US-11-087-099-2298
7	34	97.1	475	11	US-11-087-099-7571
8	34	97.1	475	11	US-11-188-298-6764
9	34	97.1	476	11	US-11-087-099-1256
10	34	97.1	478	11	US-11-087-099-7019
11	34	97.1	478	11	US-11-087-099-9555
12	34	97.1	478	11	US-11-188-298-8872
13	34	97.1	482	11	US-11-087-099-4146
14	34	97.1	491	11	US-11-087-099-9097
15	33	94.3	119	11	US-11-250-411-97
16	33	94.3	119	11	US-11-250-411-101
17	33	94.3	138	11	US-11-250-411-86
18	33	94.3	138	11	US-11-250-411-90
19	33	94.3	441	11	US-11-087-099-2305
20	33	94.3	456	11	US-11-087-099-8799
21	33	94.3	474	11	US-11-087-099-10672

22	94.3	1023	9	US-10-995-561-968	Sequence 968, Ap
23	91.4	122	9	US-10-467-657-5906	Sequence 5906, Ap
24	91.4	445	11	US-11-079-463-8428	Sequence 8428, Ap
25	91.4	480	11	US-11-079-463-7586	Sequence 7586, Ap
26	91.4	566	11	US-11-188-298-3470	Sequence 3470, Ap
27	91.4	586	11	US-11-079-463-10025	Sequence 10025, A
28	88.6	10	11	US-11-129-741-3641	Sequence 3641, Ap
29	85.7	16	9	US-10-929-988-81	Sequence 81, Appl
30	85.7	2335	9	US-10-821-234-1610	Sequence 1610, Ap
31	82.9	347	9	US-10-506-454-1117	Sequence 1117, Ap
32	82.9	400	9	US-10-467-657-7096	Sequence 7096, Ap
33	82.9	488	11	US-11-087-099-7125	Sequence 7125, Ap
34	80.0	8	11	US-11-045-024-4376	Sequence 4376, Ap
35	80.0	8	11	US-11-045-024-4377	Sequence 4377, Ap
36	80.0	8	11	US-11-045-024-12720	Sequence 12720, A
37	80.0	8	11	US-11-045-024-12755	Sequence 12755, A
38	80.0	9	11	US-11-045-024-262	Sequence 262, App
39	80.0	9	11	US-11-045-024-263	Sequence 263, App
40	80.0	9	11	US-11-045-024-4500	Sequence 4500, Ap
41	80.0	9	11	US-11-045-024-4501	Sequence 4501, Ap
42	80.0	9	11	US-11-045-024-6570	Sequence 6570, Ap
43	80.0	9	11	US-11-045-024-6641	Sequence 6641, Ap
44	80.0	10	11	US-11-045-024-2129	Sequence 2129, Ap
45	80.0	10	11	US-11-045-024-2130	Sequence 2130, Ap

ALIGNMENTS

RESULT 1
US-11-087-099-1003
; Sequence 1003, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1003
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Oenococcus oeni
US-11-087-099-1003
Query Match 97.1%; Score 34; DB 11; Length 464;
Best Local Similarity 57.1%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GYWXWXXW 7
Db 94 GYWLSSW 100
RESULT 2
US-11-087-099-11321
; Sequence 11321, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11321
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis subsp. subtilis str. 168
US-11-087-099-11321
Query Match 97.1%; Score 34; DB 11; Length 469;

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Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 97 GYWASW 103

RESULT 3
US-11-188-298-19864
; Sequence 19864, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19864
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Bacillus cereus ATCC 14579
US-11-188-298-19864

Query Match 97.1%; Score 34; DB 11; Length 471;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 92 GYWLSW 98

RESULT 4
US-11-087-099-12291
; Sequence 12291, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12291
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-087-099-12291

Query Match 97.1%; Score 34; DB 11; Length 472;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 94 GYWISW 100

RESULT 5
US-11-087-099-1870
; Sequence 1870, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464

Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 93 GYWISW 99

RESULT 6
US-11-087-099-2298
; Sequence 2298, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2298
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-087-099-2298

Query Match 97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 93 GYWISW 99

RESULT 7
US-11-087-099-7571
; Sequence 7571, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7571
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-087-099-7571

Query Match 97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 93 GYWISW 99

RESULT 8
US-11-188-298-6764
; Sequence 6764, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
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; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6764
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Lactobacillus sakei
US-11-188-298-6764

Query Match 97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 94 GYWLSAW 100

RESULT 9
US-11-087-099-1256
; Sequence 1256, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1256
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-11-087-099-1256

Query Match 97.1%; Score 34; DB 11; Length 476;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 95 GYWLSAW 101

RESULT 10
US-11-087-099-7019
; Sequence 7019, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7019
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-087-099-7019

Query Match 97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 98 GYWLSAW 104

RESULT 11
US-11-087-099-9555
; Sequence 9555, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9555
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-087-099-9555

Query Match 97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 96 GYWLSAW 102

RESULT 12
US-11-188-298-8872
; Sequence 8872, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8872
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-188-298-8872

Query Match 97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
|||
Db 96 GYWLSAW 102

RESULT 13
US-11-087-099-4146
; Sequence 4146, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4146
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-087-099-4146

Query Match 97.1%; Score 34; DB 11; Length 482;

Best Local Similarity 57.1%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 103 GYWFAYW 109
Search completed: May 2, 2006, 09:33:43
Job time: 11.3488 secs

QY 1 GYWXW 7
Db 94 GYWISAW 100

RESULT 14

US-11-087-099-9097
; Sequence 9097, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9097
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens Pfo-1
US-11-087-099-9097

Query Match 97.1%; Score 34; DB 11; Length 491;
Best Local Similarity 57.1%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 109 GYWISAW 115

RESULT 15

US-11-250-411-97
; Sequence 97, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-97

Query Match 94.3%; Score 33; DB 11; Length 119;
Best Local Similarity 57.1%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 94 GYWISAW 100